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Journal:	*Annals of Oncology*
Manuscript ID	ANNONC-2018-1554.R1
Manuscript Type:	Original Article
Date Submitted by the Author:	22-Oct-2018
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Keywords:	glioblastoma, evolution, residual disease, infiltration, sub-ventricular zone
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Evolutionary dynamics of residual disease in human glioblastoma

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Abstract

Glioblastoma is the most common and aggressive adult brain malignancy against which conventional surgery and chemoradiation provide limited benefit. Even when a good treatment response is obtained, recurrence inevitably occurs either locally (c.80%) or distally (c.20%), driven by cancer clones that are often genomically distinct from those in the primary tumour. Glioblastoma cells display a characteristic infiltrative phenotype, invading the surrounding tissue and often spreading across the whole brain. Cancer cells responsible for relapse can reside in two compartments of residual disease that are left behind after treatment: the infiltrated normal brain parenchyma, and the sub-ventricular zone (SVZ). However, these two sources of residual disease in glioblastoma are understudied because of the difficulty in sampling these regions during surgery. Here we present the results of whole-exome sequencing of 69 multi-region samples collected using fluorescence-guided resection from 11 patients, including the infiltrating tumour margin (M) and the SVZ for each patient, as well as matched blood. We used a phylogenomic approach to dissect the spatio-temporal evolution of each tumour and unveil the relation between residual disease and the main tumour mass. We also analysed two patients with paired primary-recurrence samples with matched residual disease. Our results suggest that infiltrative subclones can arise early

during tumour growth in a subset of patients. After treatment, the infiltrative subclones may seed the growth of a recurrent tumour, thus representing the 'missing link' between the primary tumour and recurrent disease. These results are consistent with recognised clinical phenotypic behaviour and suggest that more specific therapeutic targeting of cells in the infiltrated brain parenchyma may improve patient's outcome.

Key words: glioblastoma, tumour margin, subventricular zone, cancer evolution, phylogenetics

Key message: In this study we investigate the evolution of residual disease in glioblastoma that is left behind after surgery, in particular cancer cells in the infiltrative tumour margin and in the subventricular zone. We found that residual disease samples contained early precursor cancer clones that were involved in the development of the disease and may contribute to recurrence.

Introduction

Glioblastoma (GB) is a lethal brain cancer against which effective therapeutic options are lacking [1]. The disease is characterised by variegated clinical phenotypes[2-4] and intra-tumour heterogeneity (ITH) [5-7]. The disease aetiology and clinical course have distinct features compared to other cancers. Unlike other solid tumours, glioblastoma rarely metastasises outside the brain, but it invariably recurs, limiting the median survival to approximately 14 months [1]. In approximately 80% of aggressively treated patients, disease progression/recurrence occurs within 2cm of the resection margin. In the remaining patients, even when complete surgical removal of the primary lesion was possible, the tumour recurs distally [6-8] and even drastic hemispherectomy procedures fail to eradicate the disease [9]. Cancer cells from these distal recurrent lesions, despite sharing a common ancestor with the primary tumour, are often genomically distinct [6-8]. Moreover, at diagnosis glioblastoma already displays a characteristic infiltrative phenotype, invading the surrounding brain tissue and often diffusely infiltrating the whole brain [10]. We have previously shown that malignant clones present in the sub-ventricular zone (SVZ), a known neural stem cell germinal niche, often contain tumour precursor cells [11], a finding that has been recently corroborated [12]. Indeed, infiltration is ubiquitous in glioblastoma, with cells migrating through diverse regions of the brain microenvironment including white matter tracts [13] and blood vessels [14]. In addition, up to 10% of glioblastoma cases present as multifocal disease at diagnosis [15], a rare occurrence in other solid tumours.

The accumulating clinical and genomic evidence suggests that infiltration may be a very early event in glioblastoma development, so that no matter how early a cancer is detected, it has already spread to distal regions of the brain, including the normal brain parenchyma and the SVZ (Figure 1A). After treatment (Figure 1B), infiltrative cells in the brain parenchyma and in the SVZ can drive relapse. Thus, even in the case of optimal surgery and when the tumour mass has been macroscopically resected, residual disease will trigger new growth, giving rise to recurrence, either locally or distally (Figure 1C). We argue that the recent seminal studies performed on primary-recurrent matched glioblastoma samples [6-8] point at the infiltrative population as the "missing link", connecting the primary and the recurrent malignant clone in the evolution of the disease.

Methods

Patient cohort and samples

Sixty-nine tissue samples were collected from neurosurgical fluorescence-guided resections performed on ten IDH1 wildtype glioblastoma patients and one IDH1 mutant anaplastic astrocytoma patient (see Table S1 for clinical information). Between 5 and 9 multiple samples from the tumour mass (T, at least 1cm apart), sub-ventricular zone (SVZ) and infiltrative margin (M) areas were collected from each patient (Figure 2). Tumour mass samples were numbered as the surgery progressed and hence T4 samples tend to be deeper into the resection cavity than T1 samples. SVZ samples are taken after T4. In the case of the two primary/recurrence cases, 3 samples (T, SVZ, M) were taken during the primary and secondary surgical resections for a total of 6 specimens per patient. Thirty 10-um cryosections were taken from each frozen tissue for DNA extraction using the DNeasy Blood & Tissue kit (Qiagen). Patient informed consent was obtained and tissue collection/storage protocols were compliant with the UK Human Tissue Act 2004 and approved by the Local Regional Ethics Committee (LREC ref 04/Q0108/60). No difference in 5-ALA labelling capacity was observed between patients.

Whole-exome and targeted sequencing

Between 100-300ng of DNA from each of the 69 tumour specimens and 11 blood samples were used for whole exome sequencing using the Agilent SureSelectXT Human All Exon V5 Kit. Median coverage was 157X (min. 108X, max. 187X). A custom targeted sequencing panel for 891 SNVs (covered by a total of 5,090 amplicons) identified from the exome sequencing data was designed using Agilent's Haloplex technology (TES1). In addition, we designed a separate Agilent SureSelect XT2 capture panel to specifically validate 1,054 SNVs found in the M and SVZ samples across all patients (TES2). Both amplicon (TES1) and targeted capture (TES2) libraries were sequenced on an Illumina HiSeq2500 obtaining a median coverage of 4,050X and 1,128X respectively in reported variants (Figure 3A and S1). Copy number alterations per sample are reported in Figure 3B. See Supplementary Material and Methods for details about bioinformatics analysis.

Results

Intra-tumour heterogeneity in the tumour mass and residual disease

We performed fluorescence-guided multi-region sampling of different regions from primary tumours (T1, T2, T3, …; Figure 2A) and also collected samples from the infiltrative margin M (*n*=11; Figure 2B) and the SVZ (*n*=15; Figure 2C). The margin is defined by non-fluorescent tissue beyond the fluorescent tumour mass. We previously reported that this area appears histologically as normal brain and is composed by only 5-10% of tumour cells [16]. The tumour mass and SVZ samples displayed high tumour content (median 58.5% and 22.1% respectively). The SVZ samples are fluorescent and we demonstrated contain cancer clones [11]. Clinical and follow-up information, as well as imaging was available (Table S1). Samples from the tumour mass and SVZ from 7/11 patients were common to our previous studies, for which we had performed microarray copy number profiling and gene expression alone [5, 11]. The margin samples are presented here for the first time.

In the present study, multi-region whole-exome sequencing (see Material and Methods) identified extensive intra-tumour heterogeneity at the level of single nucleotide variants (SNVs). Heterogeneity at the level of SNV putative drivers (from ref [4]) was evident in 5/11 patients, especially in EGFR, PIK3R1 and TP53 (Figure 3A and S1). Copy number profiles inferred from the whole-exome sequencing confirmed the heterogeneity levels reported in previous studies (Figure 3B and S2). Copy number events were highly recurrent, especially EGFR amplification (SP42, SP54, SP55, A23 and A34), chromosome 10 loss containing PTEN (all patients), and CDKN2A homozygous deletion (SP42, SP52, SP55, SP56, SP57 and A44), corroborating the findings from large scale studies [2]. Our custom Targeted panel TES1 (see Material and Methods) confirmed the results from exome sequencing (Figures 3A and S1). See Table S2 for purity estimations, Table S3 for copy number states and Supplementary Data for VCF files with SNV calls.

Because the infiltrative margin (M) samples consist of scattered cancer cells in the surrounding normal brain, the purity of those samples was expectedly low (5-10%). Purity is a confounding factor for calling mutations, leading to possible false negatives that may impact the phylogenetic analysis [17]. To tackle this problem, we designed a second targeted sequencing panel (TES2) specifically to validate whether mutations that were present in all the other tumour samples were really absent from the infiltrative areas (indicating the margin or SVZ as an ancestral subclone). This panel confirmed that several mutations that appeared truncal to the tumour mass (putative truncal) were not present in the margin sample (Figure 3A and S1, *TES2* panel). In addition, to further support our results, we developed a statistical method to test whether genomic variants in targeted sequencing that are not found in the margin are likely to be truly absent, rather than being false negatives (i.e. in the second case, if there is no power to determine with reasonable certainty that the mutation is not present).

Our test scans mutations that were identified as “putatively truncal” from the tumour mass samples (T1, T2, …). These mutations have high cancer cell fraction (CCF) in all T samples (Figure 4A, representative example of patient SP52). We reasoned that if the cancer subclones in the margin were just infiltrative cells deriving from the tumour mass – rather than an early ancestor – then “putative truncal” mutations should also be found in the margin (“truly truncal”). However, a failure to identify these mutations in the margin, despite the very high depth of sequencing of targeted panels, may occur as a false negative owing to low purity. Similar to previous approaches [18], our statistical method accounts for the confounding factor of purity, and tests the null hypothesis that “putative truncal” mutations are present in the margin, but miss to be detected in the margin. Rejecting the null indicates that these mutations are unlikely to be present in M.

We first fit a beta-binomial distribution to the set of putative truncal mutations, separated by copy number state (Figure 4B, see Supplementary Material and Methods for details). This provides the expected variant allele frequency of a mutation in a high purity sample, such as T1-4. This model allows calculation of the expected frequency of a mutant given any purity value, for example the 5% purity of the margin sample. We then examine the whole-exome and targeted sequencing data (TES1 and TES2) from margin samples and consider those putative truncal SNVs that were not detected by any assay (Figure 4C). Given the coverage achieved at the locus of the missing mutation, and the beta-binomial model trained on putative truncal SNVs, we can calculate the likelihood of the data assuming the null is true (i.e., the mutation is *truly truncal* but 0 mutant reads are found at the locus, for a given purity). Application of our method to our dataset revealed that a considerable proportion of testable

mutations (see Supplementary Material and Methods for details) were unlikely to be present in the margin ($p < 0.05$, using Bonferroni correction), even when we assumed the margin purity to be as low as 1% (Figure 4D). These results indicate that these SNVs are likely to be absent in M, and hence cannot be truncal. The method is potentially applicable to any genomic dataset to test true negatives (see Supplementary Material and Methods and Figure S3). The results of the test for all patients are reported in Figure 3A and S1, left hand side of each heatmap. This allowed us to perform a more reliable phylogenetic analysis for each patient that included residual disease in the SVZ and the infiltrative margin M.

Evolutionary trajectories suggest early ancestor clones within residual disease

Residual disease samples diverged early from the rest of the tumour mass in the majority of patients for which M samples were available, with particular evidence for SP49, SP52, SP57, A44, SP28 for which we could apply our test (Figure 5, testable mutations that did not pass our test were excluded from the phylogeny). Importantly, residual disease was also found at recurrence, demonstrating the presence of a reservoir of cancer cells in the infiltrative margin at relapse (patients A23 and SP28). In case A23, the primary tumour mass appeared to have originated from earlier cancer cell lineages located in the margin M and SVZ collected at primary resection. However, at the time of relapse, whereas both T and SVZ appear to have acquired additional new mutations (long branch), the 'M recurrence' lineage has remained similar to the primary tumour. A comparable pattern is observed in SP28 where 'M recurrence' also shows as an early residual clone present at relapse. Hence, early ancestral clones are present both at primary and recurrence and are not generally resected. We do acknowledge that the bulk tumour mass at relapse can also be driven by incomplete resection of the primary tumour due to the neoplastic tissue extending to vital parts of the brain that cannot be removed. We note that A23 and SP28 were local recurrences and more residual disease samples from distal recurrent tumours will need to be collected in the future.

As a whole, this analysis indicates that subclones present in M may arise early during tumour growth. Moreover, in 6/11 patients, the SVZ appeared also as an early ancestor, as we previously reported [11] and as recently confirmed [12]. See Figure S4 for bootstrapping values. We do acknowledge however that in those branches some mutations may be missing due to limits of detectability. To validate further these results, we also performed single-allele methylation molecular clock analysis [19] on the same samples for a subset of patients, in particularly those where we had primary-recurrence pairs (Figure S5). Methylation molecular clock haplotyping is a single-molecule approach that allows reading the status of single CpGs in CpG island from the same DNA molecule. We have shown that some of these CpG island loci can be used for phylogenetic reconstruction, both colorectal cancer and glioblastoma [11, 19]. Importantly, because this assay is 'single-molecule', alleles that come from non-proliferative normal cells (e.g. normal contamination from neurons in the margin samples) can be discarded because of their low methylation status. Therefore, this analysis does not suffer from the problems of tumour purity of the exome analysis (see Material and Methods). Eliminating the methylation haplotypes coming from non-cancer cells allows reconstructing the tumour phylogeny orthogonally with respect to the exome trees. The results strikingly confirmed the structure of the phylogenetic trees inferred from exome sequencing, thus corroborating the results in Figure 5.

Interestingly, histopathology reports (pre WHO 2016 revision) are congruent with these phylogenetic data in multiple cases, for example SP49 GBM with low-grade areas, SP52 &

SP28 GBM with oligodendroglial component. Together these data indicate a less aggressively proliferative phenotype at early stages of the evolution of the malignancy. After the primary tumour has been treated with radio- and chemotherapy the quiescent residual subclones may trigger new growth and further clonal evolution, producing the divergence that has been observed by us and others between primary and recurrent samples in GB. This interpretation of the data is consistent with an early onset of tumour cell infiltration. Residual ancestral disease present in the SVZ and in the infiltrative margin is the source of the inevitable relapse that occurs in GB patients. This model is also consistent with the high incidence of multifocal lesions and the accumulating evidence of evolutionary divergence that is emerging from genomic data [6, 7].

Discussion

A key to understanding cancer is not just exposing intra-tumour heterogeneity, the natural process that underlines clonal evolution, but also to understand such heterogeneity in a way that is clinically relevant and therapeutically tractable. An important aspect of genomic ITH is that it embeds the evolutionary history of the tumour, a fundamental biological element that cannot be directly measured in humans. Nevertheless, inferring and understanding that history may be critical in developing a rationale for combinatorial therapeutics [20].

Specifically, in this study we leveraged the spatio-temporal decomposition of the clonal architecture of the tumour to understand the link between subclones in the main tumour mass and in residual disease left behind in the surrounding brain parenchyma and sub-ventricular zone following surgery. This residual disease is a key factor contributing to GB treatment failure because of resistance to radiation and alkylating chemotherapy coupled with an inherent ability to seed re-growth. Therefore, the main message of this study is that residual disease and not just the main tumour mass [5-8, 21, 22] must be investigated in depth from the point of view of tumour evolution if we are to understand how treatment-resistant disease develops. We acknowledge that to study the mechanisms that link residual disease to tumour relapse, additional analysis is needed, especially of primary-recurrence pairs from distal relapses where also SVZ and M would be collected. However, this remains a technical and ethical challenge.

This observation presents a challenge to the GB research community to develop the tools and strategies needed to collect and robustly analyse difficult samples from residual disease areas in prospective cohorts. Due to the limited number of patients in this study, additional analyses on larger cohorts are necessary to validate these findings. We acknowledge that analysing sparse cancer cells in the margin remains challenging, even with the most advanced sequencing and bioinformatics approaches currently available. Further work is also needed to improve purification of margin samples, which is not currently possible due to lack of reliable markers to sort GB cells. Therefore, new efforts of collecting infiltrative cells that lay distant from the main tumour mass will be needed to study residual disease with more accuracy. To do this, post-mortem efforts such as the PEACE study (Postohumous Evaluation of Advanced Cancer Environment) are likely to play a key role in revealing the biology of infiltrative disease in glioblastoma.

Acknowledgments

We acknowledge support from the NIHR tissue bank at the University of Cambridge.

Funding

This work was supported by the Schottlander Innovation Award to the Sottoriva lab. A.S. is supported by the Wellcome Trust (202778/B/16/Z), Cancer Research UK (A22909) and the Chris Rokos Fellowship in Evolution and Cancer. B.W. is supported by the Geoffrey W. Lewis Post-Doctoral Training fellowship. This work was also supported by a Wellcome Trust award to the Centre for Evolution and Cancer (105104/Z/14/Z). C.W. and S.P. is supported by The Brain Tumour Charity (10/136) & Cancer Research UK (C9221/A11869 & C9221/A16700).

Disclosure

The authors have declared no conflict of interest.

Data Access

Sequence data have been deposited at the European Genome-phenome Archive (EGA), which is hosted by the EBI and the CRG, under accession number EGAS00001003043. Further information about EGA can be found on https://ega-archive.org.

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Figure Legends

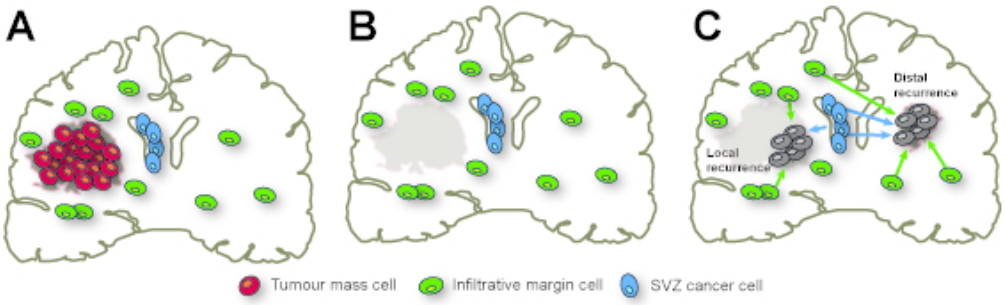
Figure 1. Residual disease in glioblastoma. (A) *At surgery, the primary tumour mass (red) only is removed (in dark grey the resection cavity).* ***(B)*** *However, infiltrative cells in the normal brain parenchyma (green) and SVZ (blue) are left behind.* ***(C)*** *Residual glioblastoma cells infiltrated throughout the brain can give rise to relapse, both locally and distally.*

Figure 2. Study design: multi-region tumour and residual disease sampling. (A) *The large majority of patients present at diagnosis with a large tumour mass that is positive for 5-ALA fluorescence. In this study, we collected multiple spatially separated regions of the tumour mass (4-6 regions per tumour in 9 patients), as well as matched primary-relapse samples in 2 patients.* ***(B)*** *Extensive infiltration is also present in the surrounding normal brain but cancer cells are so sparse beyond the resection margin that do not appear fluorescent. Samples from the non-fluorescent infiltrative margin were collected from 9/11 patients. From paired primary-recurrent patients, we collected matched margin from the primary tumour and another margin sample from the relapsed neoplasm.* ***(C)*** *In a subset of patients, disease is also found in the sub-ventricular zone (SVZ), which appears fluorescent and contains malignant clones. We collected 1-3 samples of the SVZ from all patients, including matched SVZ in primary and relapsed tumours. Through surgery and chemo-radiation, it is possible to extensively remove the primary tumour but treatment is unlikely to completely remove the infiltrative disease, nor cancer cells in the SVZ. Those represent the majority of residual disease in glioblastoma.*

Figure 3. Multi-region genomic profiles of glioblastoma residual disease. (A) *For four representative patients we report the cancer cell fractions (>80%) for the tumour mass samples and presence/absence of mutation in all the residual disease samples (see Figure S1 for all cases, Table S2 for purity and Supplementary Data for SNV calls). Putative SNV driver events are annotated. WES=whole exome sequencing; TES1=targeted amplicon sequencing panel 1; TES2=targeted exome capture sequencing panel 2. T1…4=tumour mass sample; SVZ=sub ventricular zone; M=margin.* ***(B)*** *Digital copy number alterations are reported for each sample (see Figure S2 and Table S3 for details).*

Figure 4. Testing the absence of putative truncal mutations in the infiltrative margin (representative case SP52). (A) *We detected SNVs using joint-sample variant calling from WES. We selected SNVs that had cancer cell fraction* $\mathrm{CCF} \geq 0.8$ *in all tumour mass samples (T1, T2, …) and the same CNA status across all T samples. We call these "putative truncal" SNVs. If cancer cells in M developed from T, then these mutations are "truly truncal" and should be detected also in M. However, calling these mutations in the margin might be confounded by the low purity of margin samples.* ***(B)*** *From read counts of selected SNVs, we train for every sample a Beta-Binomial model of expected Variant Allele Frequency (VAF), accounting for tumour purity and copy number status. This model describes, for each such SNV, the expected number of reads with the variant allele as a function of sample purity (i.e. we can predict how many mutant reads we expect to find in a sample like M, at purity 5%).* ***(C)*** *We use deep-sequencing data from targeted panels TES1 and TES2 to identify which putative truncal SNVs were not detected in the margin sample by any assay (missing SNVs). Based on the Beta-Binomial trained model, we created a statistical test for the null hypothesis that these mutations are truly truncal in the tumour (and hence present also in M), but remain undetected in M due to low purity.* ***(D)*** *Based on the expectation and the depth of coverage achieved for each tested mutation, we can calculate a p-value under the null. Rejecting the null means that we have evidence for the fact that these SNVs are not truly truncal, and that they are missing in the margin. This provides further evidence that the margin is ancestral to the tumour mass. The power of the test increases with higher coverage; we used a conservative setting of worst-case purity with* $\pi = 0.01$ *(1% tumour, 99% normal) for the test, and corrected it for multiple testing via Bonferroni.*

Figure 5. Phylogenetic reconstruction indicates residual disease subclones may arise early. *Phylogenetic trees built with WES data and excluding mutations that do not pass our test show the infiltrative margin sample at the top of the phylogeny, suggesting it contains cancer clones that occur early during tumour growth. In 6/11 samples the SVZ appears as an early subclone as well. Often the phylogeny recapitulates the spatial structure of the tumour, where T1, T2, … T4 samples are taken in this order as the tumour resection extends deeper into the brain. Matched samples from M and SVZ in paired primary-relapse cases A23 and SP28 show the role of residual disease in the development of glioblastoma recurrence.*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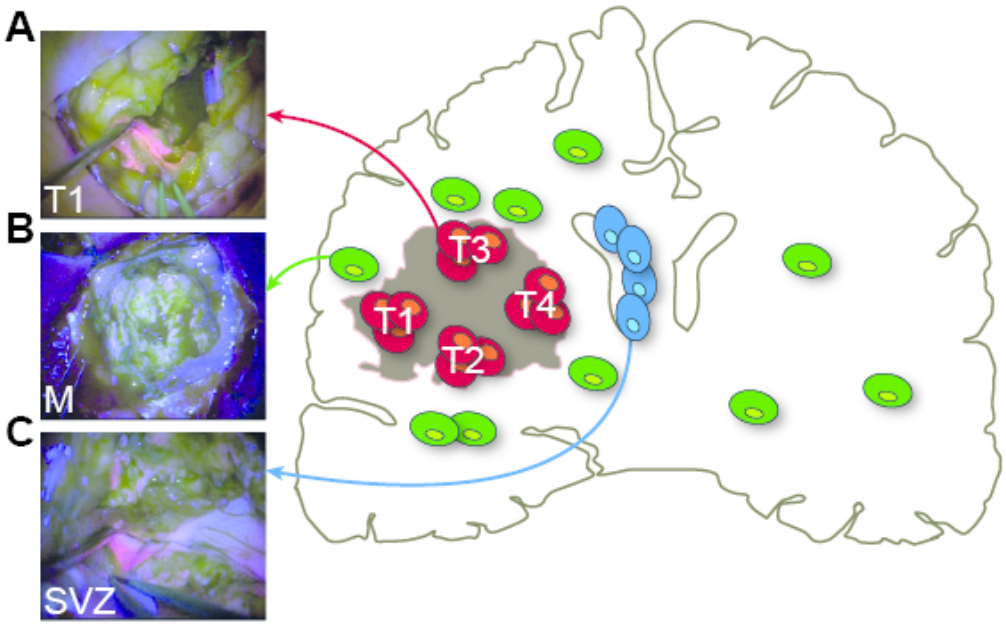
SVZ cancer cell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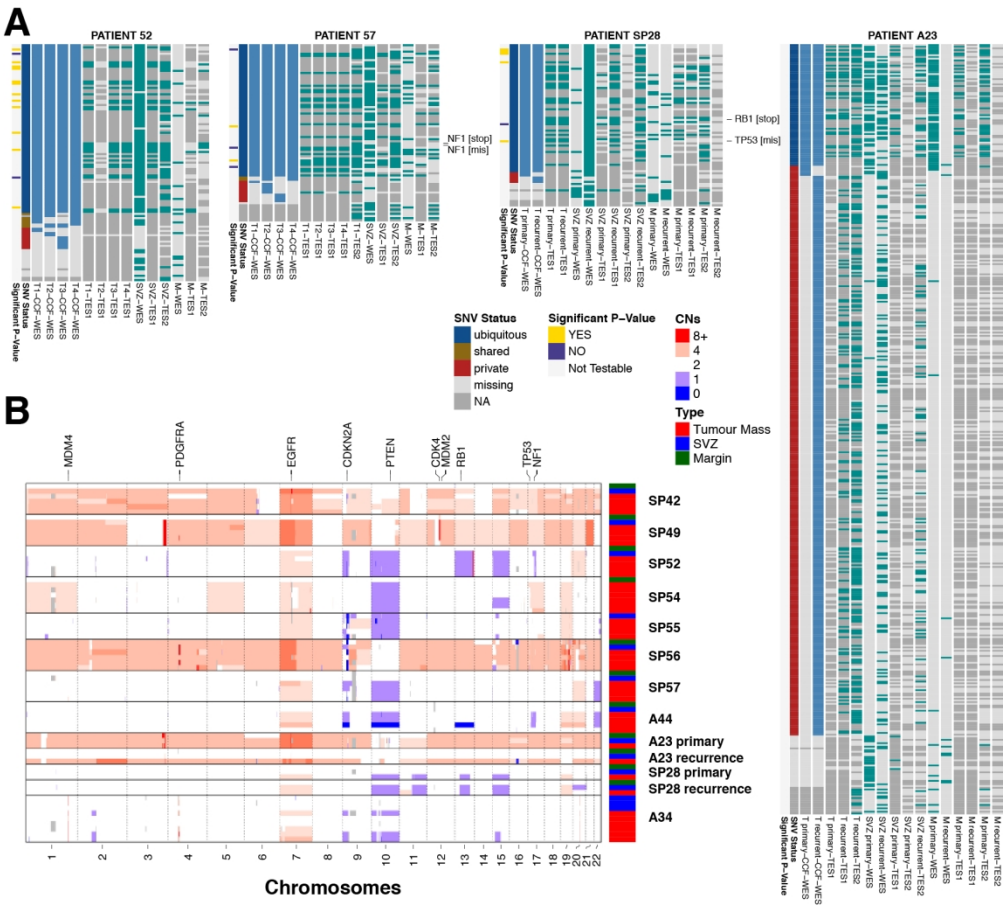
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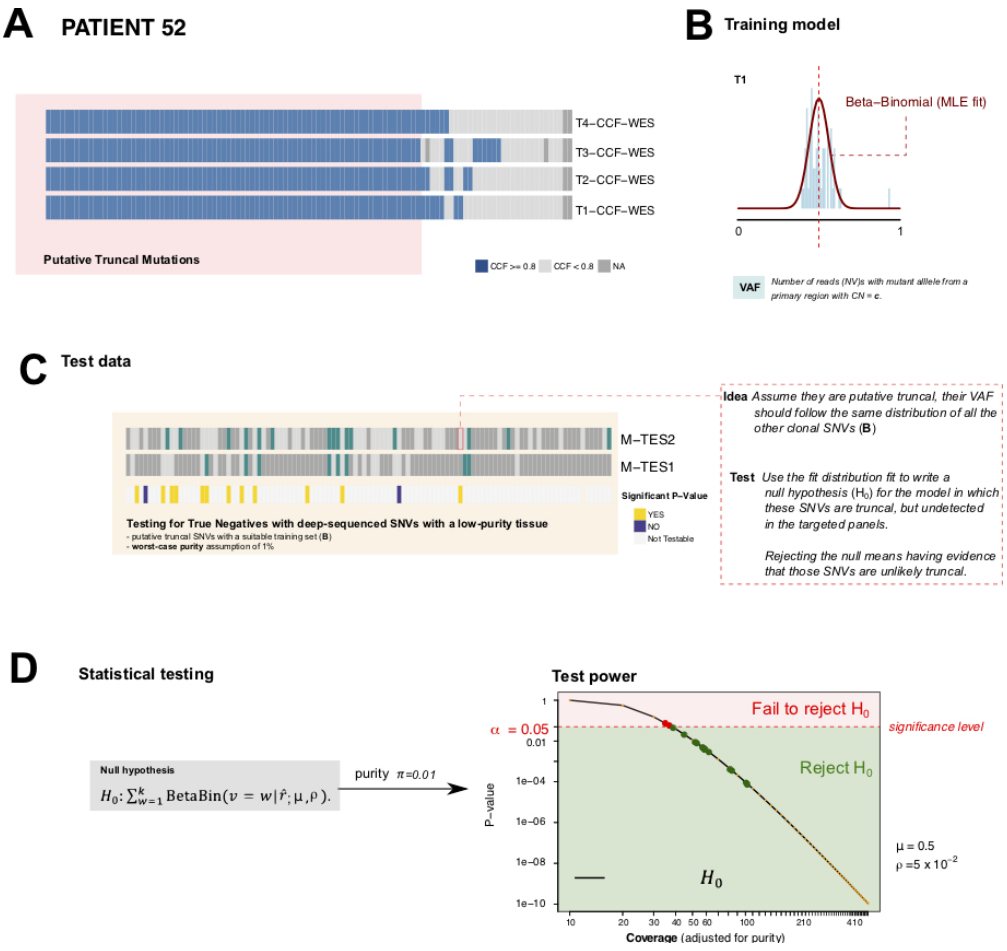
shared
private
missing
NA
Significant P−Value
YES
NO
Not Testable
CNs
8+
4
2
1
0
Type
Tumour Mass
SVZ
Margin
B
MDM4
PDGFRA
EGFR
CDKN2A
PTEN
CDK4
MDM2
RB1
TP53
NF1
SP42
SP49
SP52
SP54
SP55
SP56
SP57
A44
A23 primary
A23 recurrence
SP28 primary
SP28 recurrence
A34
Chromosomes



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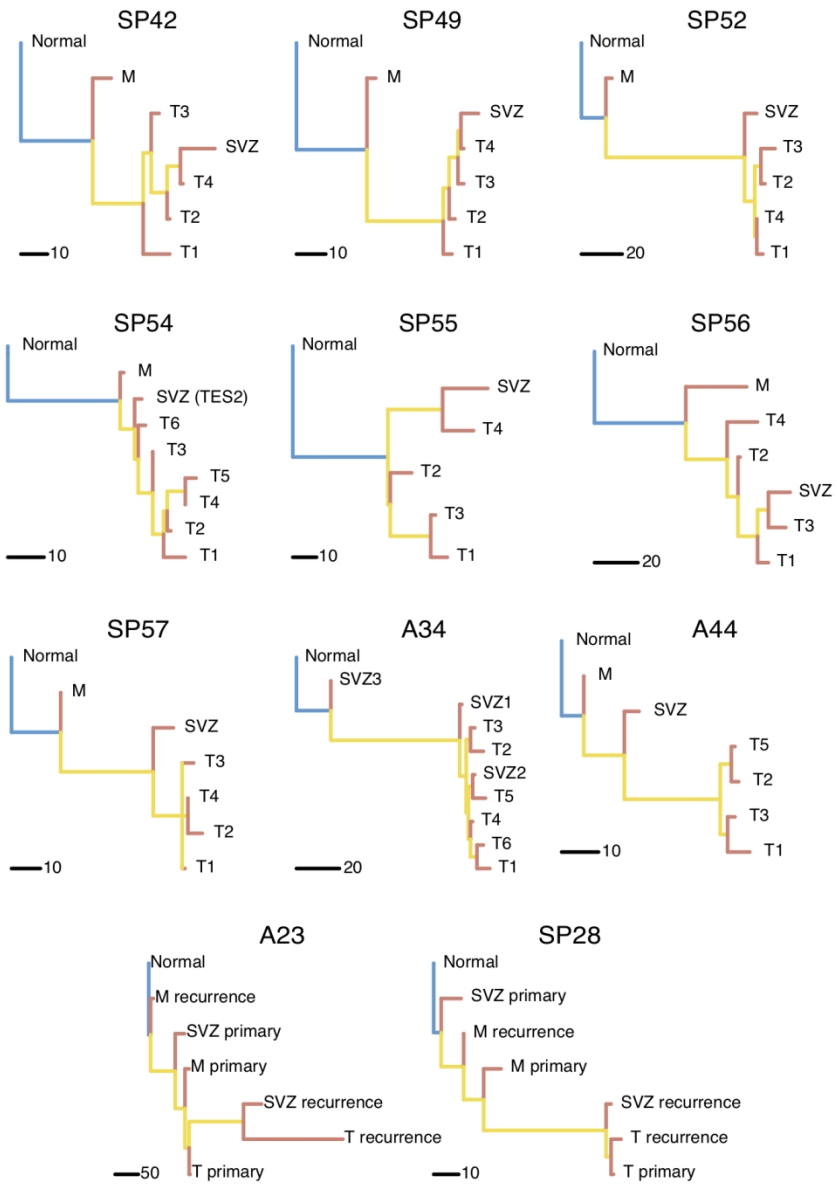

502x690mm (72 x 72 DPI)

Supplementary Material and Methods

Bioinformatics Analysis

Purity estimation: Purity estimates were gathered from a potential clonal diploid mutation (PCDM) present in the tumour mass samples and estimation by ASCAT[1] derived from the copy number solution.

Copy number analysis: Sequenza was used to identify heterozygous single nucleotide polymorphisms (SNPs) in the WES (0.4-0.6 allele frequency in the matched normal sample) and normalise depth ratios for GC content[2]. Loci were filtered for a minimum of 25 reads in the matched normal sample. Log2 ratios (LRR) were derived from the depth ratios by calculating the log (base 2) of the depth ratio and subtracting by the global median. LRR outliers were smoothed using CGHcall[3]. The mirrored allele frequencies of the heterozygous loci were segmented using piece-wise constant fitting (PCF)[4]. If BAF values in segments are considered not to be drawn from a normal distribution expected in allele balance (BAF = 0.5, Kolmogorov-Smirnov test, $p < 0.05$), a two-component Gaussian mixture model was fitted to the B-allele frequency (BAF) values of the segment utilising mixtools version 1.0.4[5], in order to estimate BAFs representative of the major allele (code available as an R package at, www.github.com/georgecresswell/MiMMAl). Major allele BAF and the LRR of the genome segments were used as input for ASCAT to estimate tumour purity and ploidy, limiting the minimum purity of the solution to the lower 95% binomial confidence limit (Wilson method) of a PCDM purity estimate adjusted for a tetraploid solution. Ploidy parameter space was restricted in tumours manually determined to have high ploidy states, additionally purity and ploidy was preset if a solution was not determined. The purity and ploidy of the ASCAT solution was used to assess the clonality of each segment using the Battenberg methodology[6]. If a segment was considered subclonal, the copy number state with the highest prevalence was taken.

Identification and validation of somatic variants: adapter trimming was performed with Skewer v0.1.126[7] specifying criteria on the length and quality of the reads (minimum of 35 after trimming and mean of 10 before trimming accordingly). Then, Burrows-Wheeler Aligner (BWA) v0.7.12[8] was used to map the reads to human reference genome hg19, and PCR duplicates were flagged using Picard tools. Mutation calling was performed in two ways: 1) with Mutect2[9] on single tumour-normal pairs 2) with Platypus v0.8.1[10], carrying out joint mutation calling among all samples from the same patient. All mutations derived from step (1) with Mutect2 were accessioned as biased prior ('source') option in Platypus run, to benefit from both mutational calling methods and explore a wider range of true positive calls. Somatic variants in WES samples were filtered as follows: i) variants in segmental duplicated regions and centromeric regions were removed ii) only specific Platypus FILTER field was considered (PASS, alleleBias, Q20, QD, SC and HapScore), iii) a minimum value of 10 was accepted for coverage and genotype quality, iv) minimum of 3 reads coverage on the alternative variant in at least

one of the tumour samples per patient to allow for variants in low allele frequencies to be identified, v) None of the reads covering the alternative variant should be present in the germline sample, and vi) genotype in the germline sample should be homozygous to the reference (0/0) . Mutations with a Variant Allele Frequency (VAF) <=5% were excluded. Somatic variants were annotated both with CAVA[11] and VEP[12]. SNV calling on the targeted capture samples was performed using Platypus in genotyping mode. Somatic SNVs were filtered based on i) genotype quality, minimum of 10 ii) total coverage, minimum of 300 and iii) coverage on the alternative variant, minimum of 10. Somatic mutations that failed to be validated in all samples per patient were excluded from the analysis. In any other case, VAF is indicated as NA in the failed sample. All somatic mutation calls from TES and WES panels are available in VCF files as Supplementary Data.

Driver genes: the complete set of SNVs was compared to a list of known putative driver genes in glioblastoma from ref[13].

Cancer cell fraction estimation: Cancer cell fraction of each variant is calculated using the VAF, estimated purity of the sample and total copy number state of the segment in which the variant belongs[14]. The estimated purity calculated by ASCAT was used unless the estimation was 1, then the PCDM purity estimate was used. To avoid overcalling subclonality, the number of mutated alleles was assumed to be 1.

Phylogenetic reconstruction: for each patient, SNVs identified from the whole exome sequencing panel were used to construct sample phylogenies using PAUP* (version 4.0a) with the maximum-parsimony criterion[15]. CCF values for the SNVs were first dicotomised to produce tables indicating the presence/absence of each mutation in each sample by defining a mutation as present where CCF≥0.2. For patient 54, the SVZ sample was included in the phylogenetic analysis with mutations identified by the TES2 panel and dicotomised as above. For all patients, we considered only mutations for which the presence/absence in each sample was determined. Where a mutation was absent from a margin sample (M) for a patient, but not identified as a true negative with high probability, this mutation was omitted from the phylogenetic reconstruction. The maximum-parsimony trees were identified via a heuristic search with default settings. For each phylogenetic tree, 1000 replicates of bootstrap analysis were carried out to assess the support (Figure 5). Trees were rendered with the R package *phytools*[16] (R version 3.3.2, phytools version 0.6-44).

Molecular Clock Analysis

Molecular clock phylogenetic reconstruction: FASTQ files were trimmed to remove adaptor sequences using Skewer v0.1.126 [7]. Paired reads were then aligned to hg19 using Bismark v0.18.2 [17]. Bismark methylation extractor was then used to extract methylation states of possible CpG sites from the original top and bottom strands. For each molecular clock loci called CpGs are identified. CpGs are used for analysis if they have a total number of calls for a position (methylated plus unmethylated) greater than or equal to the value at which the cumulative density function equals 0.05 for a Poisson

distribution where λ is equal to the maximum CpG count in the clock region. Reads with a call missing for a genomic position that passes this coverage filter are removed to leave only complete reads with a methylation call on all locations. In each tumour sample reads are required to have at least 2 methylated CpG sites and reads can only have a maximum of 80% methylation, to remove reads that are likely produced by cells that have a low turnover (normal cells) and clocks that have reached saturation and are therefore non-informative, respectively. Remaining haplotypes (reads) with an overall abundance of 1% or less are removed due to their rarity. For each tumour sample 100 random haplotypes are selected with replacement and an additional set of 100 'synthetic' unmethylated haplotypes are created as a reference for each case.

A similarity measurement is then performed pairwise between tumour samples and the unmethylated reference as used previously[18]. In brief, the Hamming distance of each haplotype combination between the two samples is measured and the shortest distance of all these combinations is recorded and the haplotype pair is removed from consideration. This is performed iteratively until all haplotype pairs have been removed and the Hamming distances of the chosen pairs is summed. This similarity measurement between all tumour samples and the unmethylated reference is used to create a Neighbour Joining tree using phangorn v2.2.0 [19]. Trees are then rendered using the same method as the somatic mutation trees.

Method for statistical testing for mutations in the margin

Training a statistical model from read-counts: For each patient, we used its CCFs and CNA values to identify putative *clonal* SNVs in exomic regions. From Platypus VCF files, we selected only entries with:

1. A single-nucleotide mutation;
2. CCF >0.8 in *all* primary samples;
3. the *same CNA status* across all primary samples.

Mutations that do not fulfil these conditions are likely subclonal, or are not SNVs, and neglected by this analysis. Read counts for clonal SNVs are extracted from VCF files reporting Number of Variants (NV, number of reads with the alternative allele) and Reads (NR, i.e., coverage).

We corrected read counts for CNA status and tumour purity, before using them to train a statistical model for the test. Correction is carried out to estimate how many of the *observed reads* r come from the actual tumour. The correction is a standard procedure[6] which uses tumour purity π (here estimated from WES data) and tumour copy number status *c* as follows

$$\hat{r} = \frac{c * \pi}{c * \pi + 2 * (1 - \pi)} * r$$

Factor two in the correction is the diploid copy number status of normal cells. After correction, $\hat{r} < r$ is the number of reads, out of *r*, that are estimated coming from tumour cells. To be conservative, we assume the mutation multiplicity (number of allele copies that bear the mutation) is always 1.

With the corrected coverage value, we can fit a *Beta-Binomial* with number of trials $\hat{r}$, and successes NV. A success in this experiment is the detection of a read with the mutant allele; the overall Binomial sampling consists in the repetition of this experiment with $\hat{r}$ reads (i.e., the number of reads at a locus). The contribution of the Beta distribution is to capture uncertainty over the success probability of the experiment. Hence, this statistical model describes the probability of observing v mutated at coverage $\hat{r}$ as a function of the Beta distribution $B(\alpha,\beta)$

$$\mathrm{BetaBin}(v|\hat{r};\alpha,\beta) = \frac{B(v+\alpha,\hat{r}-v+\beta)\binom{\hat{r}}{v}}{B(\alpha,\beta)}$$

This quantity is related to the so-called Variant Allele Frequency (VAF), which is defined to be $v/\hat{r}$. This compound model extends Binomial sampling with over-dispersion effects that better account for non-uniform coverage in sequencing assays [20]. Technically, it is a Binomial distribution whose parameter follows a Beta distribution with hyper-parameters α and β, greater than 0.

Multiple Beta-Binomial models were trained for each copy number status for the input SNVs, and each WES sample of the primary tumour. By separating read counts by copy number status, we can adjust data for every non-diploid SNV in a more precise and consistent way. To train a model at minimum acceptable quality for the next test, we discarded all combination of parameters for which we do not have, at least, 10 available SNVs. When that is the case, we removed from downstream analysis this configuration of copy number status and input sample.

To learn the model parameters α and β from data, we used the Maximum Likelihood fitting procedure vglm for *vector generalized linear models* that is implemented in the R package VGAM (version 1.0-5).

Testing: We identified testable SNVs from two deep-sequencing targeted panels. Because panels have ~3000x coverage, we require each SNV to have at least $k = 10$ reads with the variant allele ($NV \geq 10$). When that is not the case, the SNV is considered missing from the panel, and it qualifies as suitable for our test. We particularly care about the ones that are missing in the margin sample (M): if the margin was ancestral to the primary tumour, we expect it to lack some SNVs that are clonal in the primary WES samples.

If a patient has more than one margin sample (e.g. Patient A23), we require the mutation to be absent across *all* margin samples. SNVs selected in this way appear

indeed clonal in the primary tumour but are missing in the margin biopsy from the targeted panels. Some patients have no testable mutations (e.g. Patient 42). The SNVs that we detected from both targeted panels are pooled together, and their number of reads (NR) from the VCF files is stored; if an SNV is detected from both panels, we sum the NR values from both panels.

Read counts from the margins are corrected as with the training set. Copy number status for mutations in the margin is the same for the training set, by design choice. Purity correction instead requires some considerations. Estimation of purity π for margin samples is hard because of the apparent high contamination of normal cells. To be conservative, we have used a fixed, worst-case low purity estimate of $\pi = 0.01$ (1% tumour, 99% normal). This value is much lower than the margin's likely true purity and renders the test harder since the power to reject the null decreases with coverage. Thus, a conservative purity estimate leads us to rescale observed coverage to lower values (i.e., we ``throw away'' coverage from the targeted panels).

The set of SNVs to test is divided according to the copy number status and matched to the trained models. Each group is tested independent against all models trained from the different primary regions. The null hypothesis H_0 for testing a group of SNVs is the probability of detecting NV < k (with $k = 10$) mutated reads at the corrected coverage, given the parameters μ,ρ of the matched Beta-Binomial model

$$H_0: \sum_{w=1}^{k} \text{BetaBin}(v = w|\hat{r};\mu,\rho)$$

The p-value is hence the probability of finding less than *k* reads with the variant allele at the designed locus with coverage $\hat{r}$, given the fact that we expect for a clonal SNV the number of reads to follow a Beta-Binomial model with parameters α,β (fit from WES). Thus, rejecting H_0 means rejecting the hypothesis that the SNV is present and clonal in the margin but just at lower frequency due to purity. Combined with phylogenetic analysis, this provides strong evidence of the ancestral relation between the margin and the primary, and that these missing SNVs are real *true negatives* in M. The tests are executed at confidence level $\alpha = 0.05$, and corrected for multiple testing with the stringent correction possible (Family-wise Error Rate, via Bonferroni).

Supplementary Figure and Table Legends

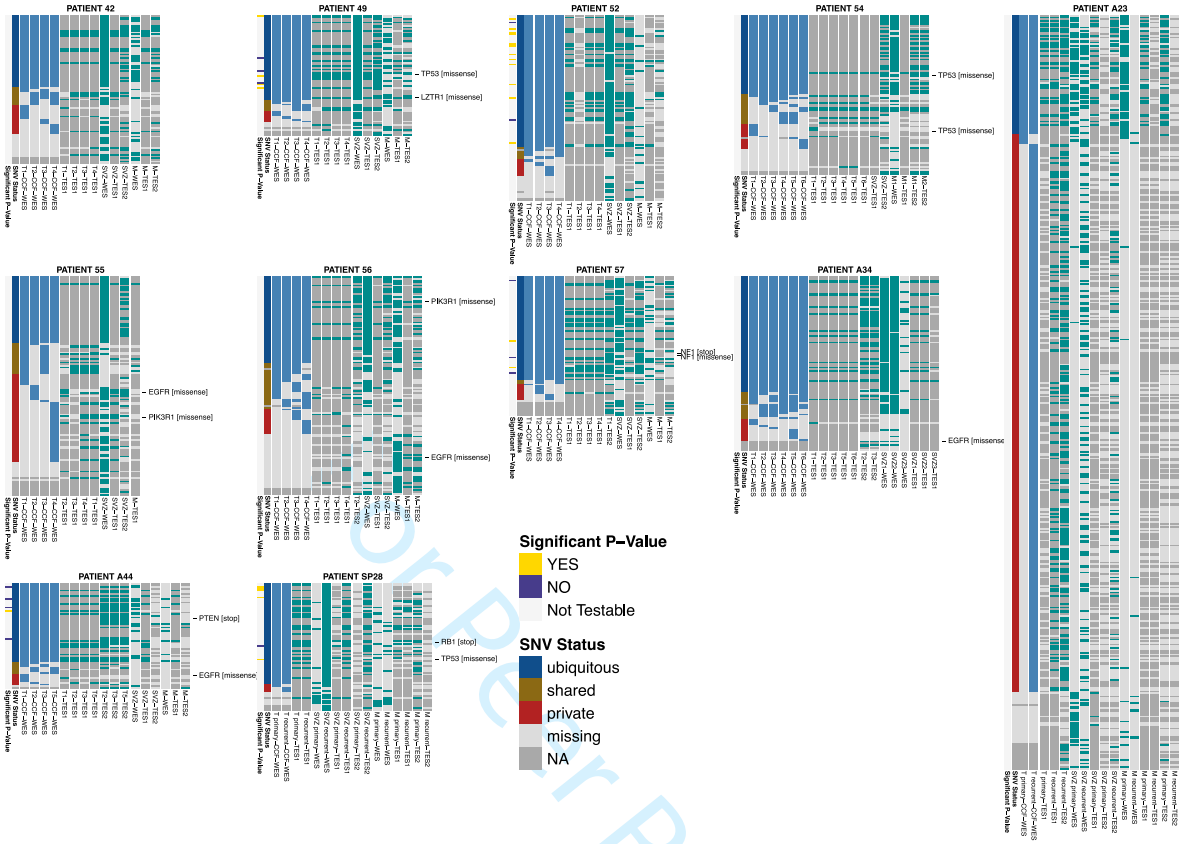

Figure S1. Multi-region SNV profiling of all patients. *For each patient we report the cancer cell fractions (>80%) for the tumour mass samples and presence/absence of mutation in all the residual disease samples for a set of representative cases (see Table S2 for purity and Supplementary Data for SNV calls). Putative SNV driver events are annotated. WES=whole exome sequencing; TES1=targeted amplicon sequencing panel 1; TES2=targeted exome capture sequencing panel 2. T1…4=tumour mass sample; SVZ=sub ventricular zone; M=margin.*

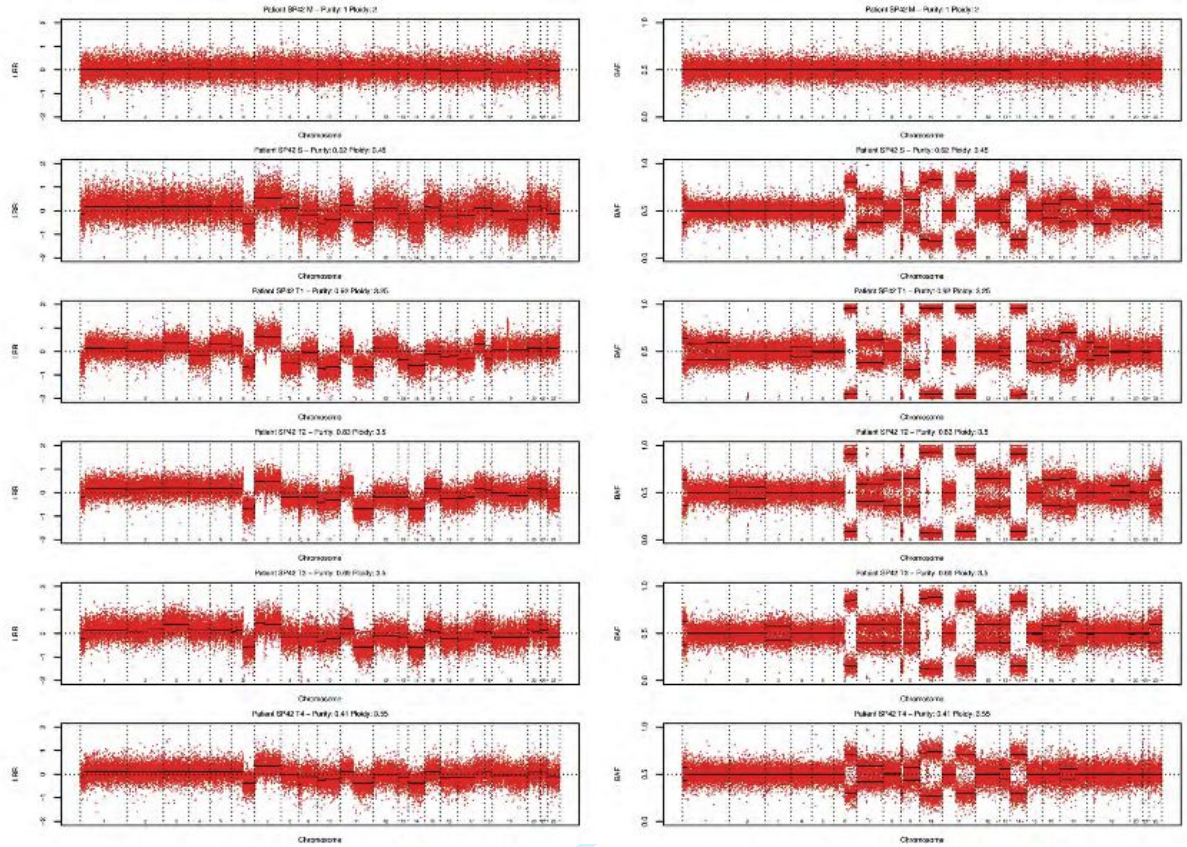

Figure S2. Log-R-ratio and B-allele-frequency profiles per sample. *For each patient and sample we report the raw LRR and BAF plots based on which the digital copy number states were estimated.*

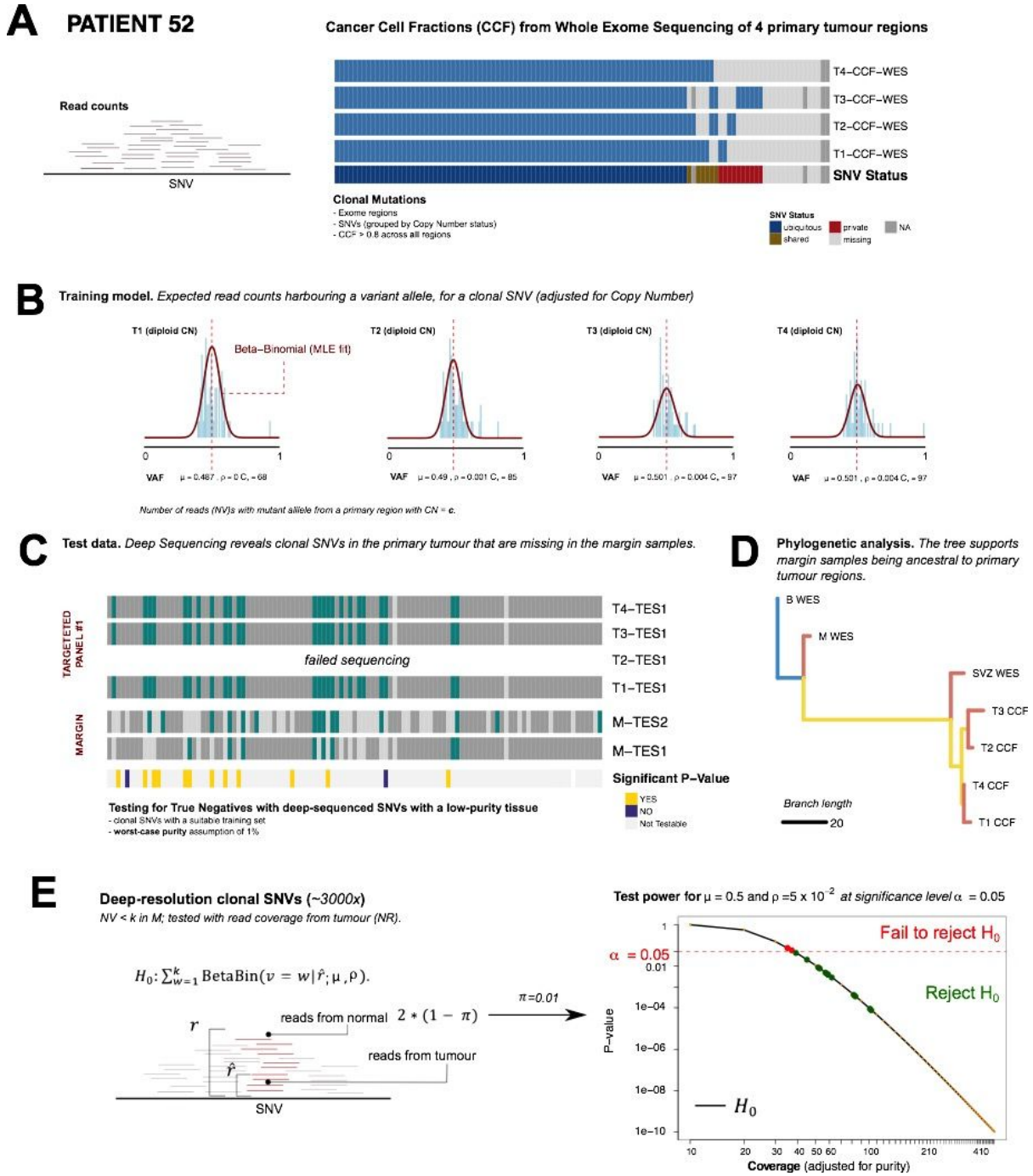

Figure S3. Margin variant testing method. (A) *We analyzed read counts to estimate CCF values from WES panels of primary tumours, margins and SVZ. We group SNVs by CN status and consider clonal those with the same CN across all samples, a CCF > 0.8.* ***(B)*** *We train a Beta-Binomial model for the frequency of the mutant allele at each SNV. The training is independent for each sample (primary tumour region), and CN status.* ***(C)*** *From deep sequencing of targeted panels, we can observe that some SNVs which are clonal in the primary tumours, are missing from margin samples. We consider them missing when they have less than k=10 reads with the variant allele: this is reasonable for a deep sequencing panel.* ***(D)*** *Phylogenetic analysis of this tumour*

suggest that the margin could contain cells that are ancestral to the primary tumour. ***(E)*** *We devised a test based on the Beta-Binomial models fit to the data for the null hypothesis that the missing SNVs in the margin – those that support early divergence – were not detected due to purity. With that we can compute exact p-values (adjusted for multiple comparison via Bonferroni) and isolate those where we can reject the null: those SNVs are unlikely clonal. The power of the test depends on the coverage at the analyzed SNVs. The higher the coverage, the less likely is that we have (by chance) observed k<10 mutant reads for a clonal SNV. We implement the test in very stringent condition: we assume purity of the sample 1% (very contaminated) and correct the observed coverage accordingly.*

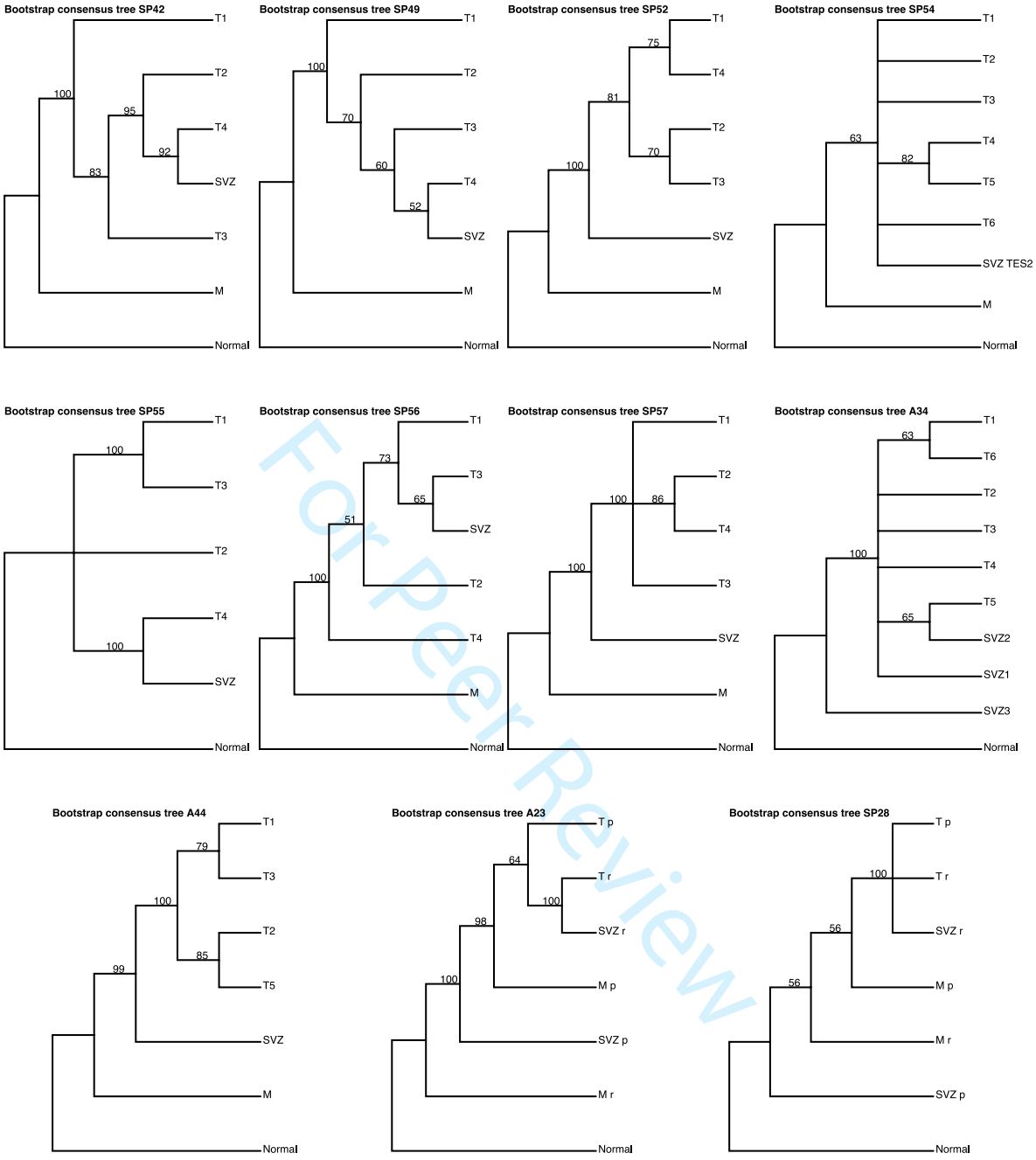

Figure S4. Phylogenetic trees bootstrapping values. *Phylogenetic bootstrapping values for WES trees (p=primary, r=relapse – e.g. Mr, SVZ p).*

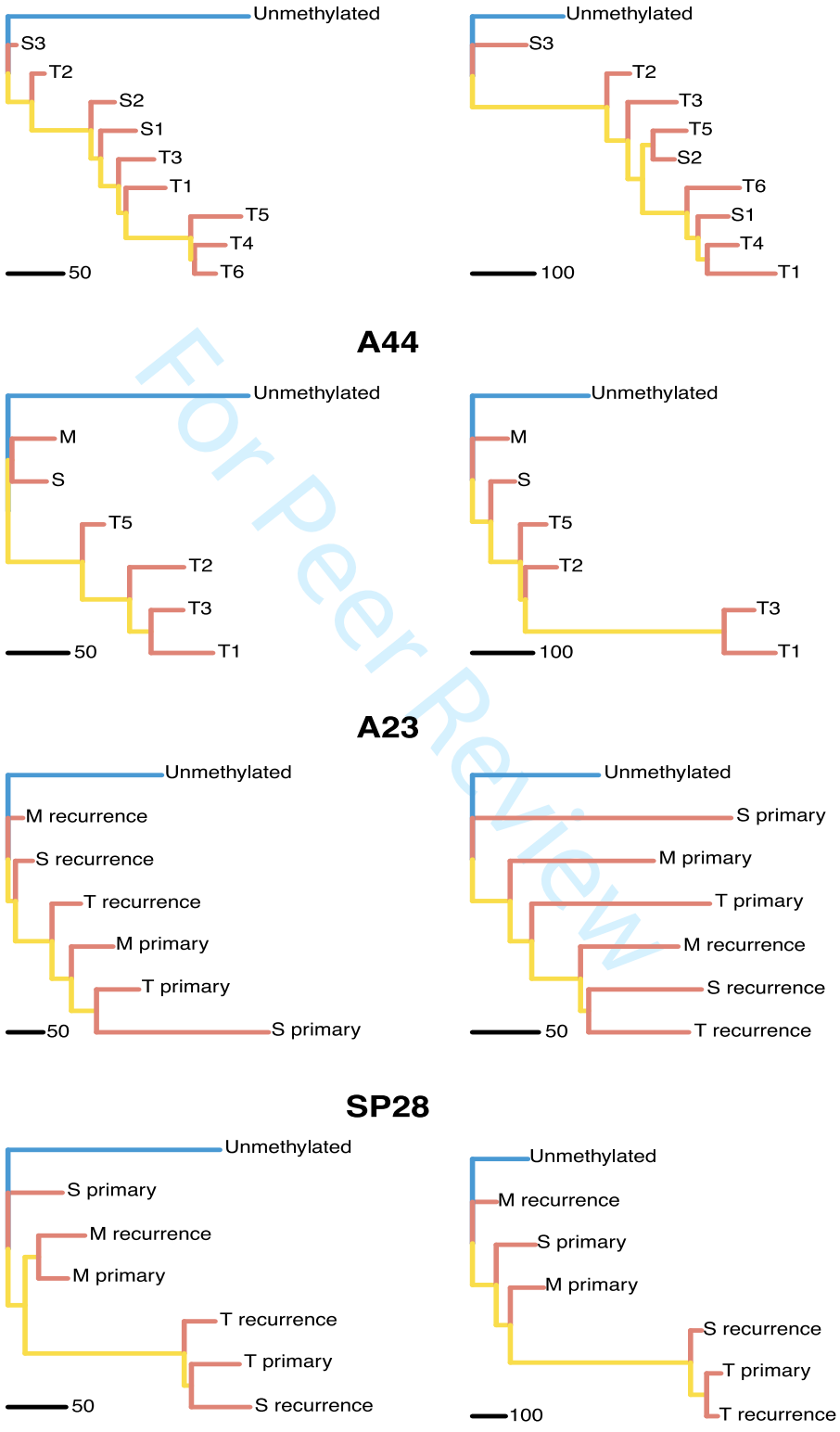

Figure S5. Phylogenetic trees using methylation clocks. *Phylogenetic trees reconstructed using single-allele methylation molecular clocks from a subset of analysed patients*

Sample ID	Survival after surgery (days)	Location	Histology	MIB	IDH1	Post op radiology	F/U
SP42	190	Lt parieto-occipital	GBM (Grade IV)	52 %	wt	Residual enhancement	radiotherapy
SP49	288	Lt temporal lobe and thalamus	GBM (Grade IV)	40 %	wt	Partial resection	radiotherapy
SP52	27	Rt Frontoparietal	GBM (Grade IV)		wt	Partial resection	radiotherapy
SP54	321	Lt frontal lobe	GBM (Grade IV)	30 %	wt	Mild enhancement post op	TMZ + radiotherapy
SP55	298	Left temporal	GBM (Grade IV)		wt	Residual tumour	
SP56	86	Rt Frontal	GBM (Grade IV)		wt		NCCU for clotting issues
SP57	354	Rt frontal	GBM (Grade IV)		wt	Good resection	Concomitant and adjuvant TMZ + radiotherapy
A34	alive	Lt frontal	Anaplastic astrocytoma	20 %	mut		Prior TMZ and radiotherapy (in 2006), re-treat with TMZ
A44	104	Rt parietal	GBM (Grade IV)	25 %	wt	Minimal residual disease	Concomitant and adjuvant TMZ + radiotherapy
A23 (primary)	1059	Lt temporal	GBM (Grade IV)	25 %	wt	Debulking	Concomitant and adjuvant TMZ + radiotherapy
A23 (recurrence)	142	Lt temporo-parietal	GBM (Grade IV)	31 %	wt	Debulking	Rre-challenge with TMZ
SP28 (primary)	588	Lt parietal	GBM (Grade IV)		wt		Gliadel, adjuvant TMZ + radiotherapy
SP28 (recurrence)	200		GBM (Grade IV)		wt		For consideration of PCV

	chemotherapy

Table S1. Clinical and follow-up information.

Table S2. Purity and ploidy estimates per sample.

Table S3. Copy number estimates per sample.

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Sample ID	Survival after surgery (days)	Location	Histology	MIB	IDH1	Post op radiology	F/U
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SP28 (primary)	588	Lt parietal	GBM (Grade IV)		wt		Gliadel, adjuvant TMZ + radiotherapy
SP28 (recurrence)	200		GBM (Grade IV)		wt		For consideration of PCV chemotherapy

Sample	PCDM.Gene	PCDM.Mutation	PCDM.lower.tetraploid	PCDM.lower	PCDM.purity	PCDM.upper	ASCAT.purity	ASCAT.ploidy	min.ASCAT.purity	max.ASCAT.purity	min.ASCAT.ploidy	max.ASCAT.ploidy
SP42M	PITX1	5_134364968	0,003417294	0,004533464	0,025641026	0,13821714	1	2	0,003417294	1	1,5	5,5
SP42S	PITX1	5_134364968	0,438622444	0,609952062	0,764705882	0,932386808	0,623,45	0,438622444	1	2,5	4,5	
SP42T1	PITX1	5_134364968	0,778064268	0,875001086	1,015706806	1,155793182	0,92	3,25	0,778064268	1	2,5	4,5
SP42T2	PITX1	5_134364968	0,499826906	0,66676475	0,837606838	1,018773638	0,83	3,5	0,499826906	1	2,5	4,5
SP42T3	PITX1	5_134364968	0,447929505	0,618907944	0,773722628	0,940880768	0,69	3,5	0,447929505	1	2,5	4,5
SP42T4	PITX1	5_134364968	0,257866457	0,409607576	0,554621849	0,727491568	0,41	3,55	0,257866457	1	2,5	4,5
SP49M	ZNF469	16_88498626	0,005518529	0,008941017	0,032520325	0,114700873	1	2	0,005518529	1	1,5	5,5
SP49SVZ	ZNF469	16_88498626	0,23779339	0,383820973	0,514285714	0,670693622	0,57	3,45	0,23779339	1	1,5	5,5
SP49T1	ZNF469	16_88498626	0,335161492	0,501872872	0,655737705	0,830620563	0,59	3,4	0,335161492	1	1,5	5,5
SP49T2	ZNF469	16_88498626	0,123690219	0,220494522	0,366197183	0,576963445	0,39	3,4	0,123690219	1	1,5	5,5
SP49T3	ZNF469	16_88498626	0,13748596	0,241933984	0,343949045	0,477301706	0,35	3,4	0,13748596	1	1,5	5,5
SP49T4	ZNF469	16_88498626	0,157935828	0,272782744	0,413043478	0,600356278	0,74	3,45	0,157935828	1	1,5	5,5
SP52M	FSIP2	2_186660349	0,001272673	0	0	0,022876621	1	2	0,001272673	1	1,5	5,5
SP52SVZ	FSIP2	2_186660349	0,094858661	0,173897814	0,23943662	0,325275996	0,3	1,95	0,094858661	1	1,5	5,5
SP52T1	FSIP2	2_186660349	0,285195417	0,443466404	0,542750929	0,654911089	0,58	2,05	0,285195417	1	1,5	5,5
SP52T2	FSIP2	2_186660349	0,434408432	0,605858065	0,705167173	0,811281853	0,73	2	0,434408432	1	1,5	5,5
SP52T3	FSIP2	2_186660349	0,517995827	0,682727527	0,784431138	0,891037042	0,77	2	0,517995827	1	1,5	5,5
SP52T4	FSIP2	2_186660349	0,49736365	0,664570037	0,764705882	0,870099224	0,76	2	0,49736365	1	1,5	5,5
SP54M1	OR5H1	3_97851850	0,027256086	0,05276419	0,103225806	0,197063014	1	2	0,027256086	1	1,5	5,5
SP54T1	OR5H1	3_97851850	0,235748743	0,38114927	0,515151515	0,676575808	0,63	2,25	0,235748743	1	1,5	5,5
SP54T2	OR5H1	3_97851850	0,38481754	0,555776617	0,69005848	0,837959853	0,66	2,2	0,38481754	1	1,5	5,5

SP54T3	OR5H1	3_97851850	0,162065544	0,278883719	0,403361345	0,565154757	0,69	2,35	0,162065544	1	1,5	5,5
SP54T4	OR5H1	3_97851850	0,501423113	0,668182999	0,812121212	0,964608613	0,85	2,2	0,501423113	1	1,5	5,5
SP54T5	OR5H1	3_97851850	0,378082357	0,548693517	0,694444444	0,856074261	0,88	2,15	0,378082357	1	1,5	5,5
SP54T6	OR5H1	3_97851850	0,424142147	0,595780835	0,736196319	0,888759755	0,72	2,2	0,424142147	1	1,5	5,5
SP55S	CA2	8_86388035	0,309355847	0,472254668	0,572463768	0,684410678	0,62	2,05	0,309355847	1	1,5	5,5
SP55T1	CA2	8_86388035	0,226695342	0,369216999	0,460431655	0,56635479	0,55	2,1	0,226695342	1	1,5	5,5
SP55T2	CA2	8_86388035	0,68676232	0,814273309	0,94017094	1,068001211	0,87	2,1	0,68676232	1	1,5	5,5
SP55T3	CA2	8_86388035	0,174006049	0,296290299	0,386554622	0,496307126	0,35	2,15	0,174006049	1	1,5	5,5
SP55T4	CA2	8_86388035	0,499320154	0,666313847	0,787878788	0,916383345	0,67	2,1	0,499320154	1	1,5	5,5
SP56M	PIK3R1	5_67589138	0,281843965	0,43938943	0,541832669	0,658088661	0,4	3,75	0,281843965	1	3	5
SP56S	PIK3R1	5_67589138	0,110783562	0,199947437	0,2734375	0,368410355	0,17	3,95	0,110783562	1	3	5
SP56T1	PIK3R1	5_67589138	0,327077256	0,492716613	0,606334842	0,733404757	0,47	4,05	0,327077256	1	3	5
SP56T2	PIK3R1	5_67589138	0,033132842	0,064119837	0,108786611	0,181649225	0,1	4	0,1	0,1	4	4
SP56T3	PIK3R1	5_67589138	0,144688654	0,252922815	0,337552743	0,443314944	0,31	4,05	0,144688654	1	3	5
SP56T4	PIK3R1	5_67589138	0,188205583	0,316551989	0,436619718	0,58636628	0,61	3,9	0,188205583	1	3	5
SP57M	TRAK2	2_202262283	0,001272673	0	0	0,049617962	1	2	0,001272673	1	1,5	5,5
SP57S	TRAK2	2_202262283	0,01028518	0,018819203	0,048192771	0,12062212	1	2	0,01028518	1	1,5	5,5
SP57T1	TRAK2	2_202262283	0,061216814	0,116011825	0,188679245	0,299625066	0,24	2,15	0,061216814	1	1,5	5,5
SP57T2	TRAK2	2_202262283	0,21528677	0,353938859	0,481751825	0,637835288	0,5	2	0,21528677	1	1,5	5,5
SP57T3	TRAK2	2_202262283	0,240067824	0,38678302	0,52991453	0,702933365	0,47	1,95	0,240067824	1	1,5	5,5
SP57T4	TRAK2	2_202262283	0,096266275	0,176232913	0,276422764	0,420440433	0,44	2,05	0,096266275	1	1,5	5,5
A23_recurrent_M	ATP10B	5_160097490	0,002302304	0,00218098	0,012345679	0,068265323	1	2	0,002302304	1	1,5	5,5
A23_recurrent_S	ATP10B	5_160097490	0,009763359	0,017745715	0,045454545	0,113942038	1	2	0,009763359	1	1,5	5,5

A23_recurrent_T	ATP10B	5_160097490	0,216092032	0,355026225	0,466666667	0,600595639	0,28	3,8	0,216092032
1	1,5	5,5							
A34S1	GANAB	11_62397228	0,096892376	0,177269474	0,271428571	0,404502418	1	2,05	0,096892376
1	1,5	3							
A34S2	GANAB	11_62397228	0,046629049	0,089517744	0,162601626	0,286407588	1	2	0,046629049
1	1,5	3							
A34S3	GANAB	11_62397228	0,002943439	0,003534864	0,02	0,108972392	1	2,05	0,002943439
1	1,5	3							
A34T1	GANAB	11_62397228	0,410114508	0,581770217	0,752293578	0,939682266	0,99	2	0,410114508
1	1,5	3							
A34T2	GANAB	11_62397228	0,010722001	0,019716366	0,057692308	0,162800802	1	2,05	0,010722001
1	1,5	3							
A34T3	GANAB	11_62397228	0,074098529	0,138671152	0,25	0,430056042	1	2,1	0,074098529
1	1,5	3							
A34T4	GANAB	11_62397228	0,170348563	0,290994897	0,427184466	0,604564923	1	2,05	0,170348563
1	1,5	3							
A34T5	GANAB	11_62397228	0,304662979	0,466744519	0,620689655	0,798952003	1	2	0,304662979
1	1,5	3							
A34T6	GANAB	11_62397228	0,532003914	0,694769977	0,872727273	1,059273934	0,76	2,05	0,532003914
1	1,5	3							
A44M	ZBED9	6_28539945	0,005532187	0,008969558	0,026315789	0,075928621	1	2,05	0,005532187
1	1,5	5,5							
A44S	ZBED9	6_28539945	0,001923597	0,001379764	0,0078125	0,043581951	1	2,05	0,001923597
1	1,5	5,5							
A44T1	ZBED9	6_28539945	0,270669965	0,425645732	0,534562212	0,659670943	0,6	2,1	0,270669965
1	1,5	5,5							
A44T2	ZBED9	6_28539945	0,176394421	0,299731151	0,394495413	0,510229794	0,34	2,1	0,176394421
1	1,5	5,5							
A44T3	ZBED9	6_28539945	0,137116782	0,241367031	0,337078652	0,460799122	0,23	2,3	0,137116782
1	1,5	5,5							
A44T5	ZBED9	6_28539945	0,030915124	0,059856825	0,106280193	0,185270096	1	2	0,030915124
1	1,5	5,5							
SP28_recurrent_M	ZNF219	14_21561310	0,006775275	0,011561406	0,033898305	0,097279331	1	2	0,006775275
1	1,5	5,5							
SP28_recurrent_S	ZNF219	14_21561310	0,347119584	0,515216743	0,644067797	0,78804037	0,53	1,85	0,347119584
1	1,5	5,5							
SP28_recurrent_T	ZNF219	14_21561310	0,172229419	0,293722021	0,408163265	0,55274896	0,49	1,95	0,172229419
1	1,5	5,5							
A23_primary_M	ATP10B	5_160097490	0,112886836	0,203329283	0,301369863	0,435231756	0,18	3,75	0,112886836
1	3	5							
A23_primary_S	ATP10B	5_160097490	0,348816349	0,517091071	0,637254902	0,770827707	0,5	3,9	0,348816349
1	3	5							
A23_primary_T	ATP10B	5_160097490	0,376029461	0,546520696	0,682926829	0,83384694	0,52	4	0,376029461
1	3	5							
SP28_primary_M	ZNF219	14_21561310	0,00260813	0,00282719	0,016	0,087849505	1	2	0,00260813
1	1,5	5,5							

SP28_primary_S	ZNF219		14_21561310	0,002363042	0,002309377	0,013071895	0,072179331
1	2		0,002363042	1	1,5	5,5	
SP28_primary_T	ZNF219		14_21561310	0,685567714	0,813435611	0,991452991	1,170013778
0,89	1,95		0,685567714	1	1,5	5,5	

patient	sample	merged_name	chr	startpos	endpos	BAF	LogR	nMajor	nMinor	clonal
SP42	M1	SP42M	1	762273	248813749	0,5	0,02445006	1	1	TRUE
SP42	M	SP42M	2	41720	242839614	0,5	0,019696926	1	1	TRUE
SP42	M1	SP42M	3	386247	197717569	0,5	0,039682578	1	1	TRUE
SP42	M	SP42M	4	60400	189065435	0,5	0,04718493	1	1	TRUE
SP42	M1	SP42M	5	163205	180670414	0,502	0,016111579	1	1	TRUE
SP42	M1	SP42M	6	335251	170892848	0,505	0,020996747	1	1	TRUE
SP42	M1	SP42M	7	286402	159025180	0,5	0,039302399	1	1	TRUE
SP42	M1	SP42M	8	280241	145750138	0,5	0,020481356	1	1	TRUE
SP42	M1	SP42M	9	286593	141008876	0,5	-0,004549274	1	1	TRUE
SP42	M1	SP42M	10	323283	135381766	0,5	-0,00080535	1	1	TRUE
SP42	M1	SP42M	11	193096	134856661	0,505	0,001777874	1	1	TRUE
SP42	M1	SP42M	12	250239	8090839	0,5	-0,007644283	1	1	TRUE
SP42	M0	SP42M	12	8386857	8386878	0,7815	-0,912025702	1	1	FALSE
SP42	M1	SP42M	12	8509668	133732624	0,505	0,026052284	1	1	TRUE
SP42	M0	SP42M	13	19042919	19529067	0,759	-0,077714185	1	1	FALSE
SP42	M1	SP42M	13	19532448	115091073	0,5065	0,010377902	1	1	TRUE
SP42	M1	SP42M	14	19118237	107283160	0,5	-0,014475786	1	1	TRUE
SP42	M1	SP42M	15	20170150	102359203	0,5	0,011899145	1	1	TRUE
SP42	M1	SP42M	16	109665	90161852	0,5	-0,05835287	1	1	TRUE
SP42	M	SP42M	17	6188	81083419	0,5	-0,027431135	1	1	TRUE
SP42	M1	SP42M	18	334994	77728221	0,5	0,012542862	1	1	TRUE
SP42	M1	SP42M	19	311708	59074653	0,5	-0,07694256	1	1	TRUE

SP42	M	SP42M	20	76962	62904542	0,5	0,005745028	1	1
TRUE									
SP42	M	SP42M	21	9825966	48078611	0,5	-0,004742163	1	
1	TRUE								
SP42	M	SP42M	22	16157827	51207915	0,5	-0,031923097	1	
1	TRUE								
SP42	S	SP42S	1	762273	11879468	0,625	-0,133396477	2	1
TRUE									
SP42	S	SP42S	1	11879685	248813749	0,503	0,180150254	2	2
TRUE									
SP42	S	SP42S	2	41720	242839614	0,504	0,162175639	2	2
TRUE									
SP42	S	SP42S	3	386247	197717569	0,5	0,169707278	2	2
TRUE									
SP42	S	SP42S	4	60400	189065435	0,5	0,169889722	2	2
TRUE									
SP42	S	SP42S	5	163205	180670414	0,5	0,14644615	2	2
TRUE									
SP42	S	SP42S	6	335251	58776982	0,5	0,18468169	2	2
TRUE									
SP42	S	SP42S	6	58777039	58778649	0,5	-2,924857267	0	0
TRUE									
SP42	S	SP42S	6	58778809	65655883	0,523	-0,546074429	1	1
TRUE									
SP42	S	SP42S	6	65767393	70071173	0,79	-0,387438336	2	0
TRUE									
SP42	S	SP42S	6	70589630	71011831	0,508	0,382622725	2	2
TRUE									
SP42	S	SP42S	6	71137992	167424293	0,807	-0,545079507	2	0
TRUE									
SP42	S	SP42S	6	167440128	167791524	0,645	-0,518014485	2	1
TRUE									
SP42	S	SP42S	6	168298875	170892848	0,8085	-0,33137124	2	0
TRUE									
SP42	S	SP42S	7	286402	54621692	0,627	0,556662093	4	2
FALSE									
SP42	S	SP42S	7	54724286	55214443	0,987	5,149326692	163	2
TRUE									
SP42	S	SP42S	7	55706275	57233554	0,504	0,015252487	2	2
TRUE									
SP42	S	SP42S	7	57528997	62694495	0,984	3,410269801	48	0
TRUE									
SP42	S	SP42S	7	62941320	65228128	0,503	0,124917995	2	2
TRUE									
SP42	S	SP42S	7	65439189	159025180	0,627	0,54709236	4	2
FALSE									
SP42	S	SP42S	8	280241	145750138	0,5	0,101303979	2	2
TRUE									

SP42	S	SP42S	9	286593	20916828	0,807177232	-0,533482579	2	0	TRUE
SP42	S	SP42S	9	20923618	141008876	0,619	-0,168157045	2	1	TRUE
SP42	S	SP42S	10	323283	46221393	0,807028291	-0,534596522	2	0	TRUE
SP42	S	SP42S	10	46960084	47416860	0,505	-0,334723744	1	1	TRUE
SP42	S	SP42S	10	47605468	51586514	0,809	-0,3725256	2	0	TRUE
SP42	S	SP42S	10	51620278	51631972	0,54	-0,29373087	1	1	TRUE
SP42	S	SP42S	10	51785694	135381766	0,8255	-0,393975075	2	0	FALSE
SP42	S	SP42S	11	193096	50381417	0,5	0,232506447	2	2	TRUE
SP42	S	SP42S	11	51411914	134856661	0,812	-0,494700811	2	0	TRUE
SP42	S	SP42S	12	250239	133732624	0,5	0,086013177	2	2	TRUE
SP42	S	SP42S	13	19042919	115091073	0,622	-0,152322569	2	1	TRUE
SP42	S	SP42S	14	19118237	20148052	0,698	-0,751716534	1	0	TRUE
SP42	S	SP42S	14	20216334	107283160	0,807397015	-0,531837231	2	0	TRUE
SP42	S	SP42S	15	20170150	20173275	0,698	-0,212729083	2	1	TRUE
SP42	S	SP42S	15	20279438	48752278	0,504	0,179590808	2	2	TRUE
SP42	S	SP42S	15	48755168	48813107	0,81	-0,168138455	2	0	TRUE
SP42	S	SP42S	15	48903126	102359203	0,5	0,137492066	2	2	TRUE
SP42	S	SP42S	16	109665	90161852	0,574	-0,216179362	2	1	FALSE
SP42	S	SP42S	17	6188	47118995	0,617	-0,200558114	2	1	TRUE
SP42	S	SP42S	17	47121551	81083419	0,5	0,116704473	2	2	TRUE
SP42	S	SP42S	18	334994	77728221	0,503	0,114596776	2	2	TRUE
SP42	S	SP42S	19	311708	24014850	0,64	-0,015953325	2	1	FALSE
SP42	S	SP42S	19	28296408	59074653	0,509	-0,399230715	1	1	TRUE
SP42	S	SP42S	20	76962	62904542	0,507	0,150332437	2	2	TRUE

SP42	S	SP42S	21	9825966	48078611	0,5	0,13088944	2	2
TRUE									
SP42	S	SP42S	22	16157827	51207915	0,571	-0,13818939	2	1
FALSE									
SP42	T1	SP42T1	1	762273	15441029	0,64	-0,50164975	2	
1	FALSE								
SP42	T1	SP42T1	1	15490865	121129557	0,585	0,137303102	2	
1	FALSE								
SP42	T1	SP42T1	1	142620901	144931392	0,517	0,149630129	2	
2	FALSE								
SP42	T1	SP42T1	1	144951880	248813749	0,591	0,117671811	2	
1	FALSE								
SP42	T1	SP42T1	2	41720	141130501	0,5	0,039036734	2	2
TRUE									
SP42	T1	SP42T1	2	141457962	141625410	0,947853287	-0,88088444		
2	0	TRUE							
SP42	T1	SP42T1	2	142012027	242839614	0,5	0,044738573	2	
2	TRUE								
SP42	T1	SP42T1	3	386247	10359628	0,5	0,386444071	2	
2	TRUE								
SP42	T1	SP42T1	3	10382111	10452231	0,6865	0,988958755	4	
2	FALSE								
SP42	T1	SP42T1	3	11076400	197717569	0,5	0,341667196	2	
2	TRUE								
SP42	T1	SP42T1	4	60400	189065435	0,554	-0,156307098	1	1
FALSE									
SP42	T1	SP42T1	5	163205	180670414	0,504	0,296288443	2	
2	TRUE								
SP42	T1	SP42T1	6	335251	65098768	0,505	0,227507947	2	
2	TRUE								
SP42	T1	SP42T1	6	65149185	65525121	0,952	-0,388952118	2	
0	TRUE								
SP42	T1	SP42T1	6	65622463	65655883	0,5	-3,926944202	0	
0	TRUE								
SP42	T1	SP42T1	6	65767393	70071173	0,945894516	-0,934082942		
2	0	TRUE							
SP42	T1	SP42T1	6	70589630	71011831	0,51	0,349733018	2	
2	TRUE								
SP42	T1	SP42T1	6	71137992	116600774	0,95541438	-0,654886609		
2	0	TRUE							
SP42	T1	SP42T1	6	116774264	116783330	0,517	-0,574300255	1	
1	TRUE								
SP42	T1	SP42T1	6	116836720	167440244	0,959	-0,684413895	2	
0	TRUE								
SP42	T1	SP42T1	6	167590541	167704944	0,568	-0,52039039	1	
1	TRUE								

SP42	T10	SP42T10 TRUE	6	167754661	167772755	0,951	-0,626843734	2
SP42	T11	SP42T11 TRUE	6	167786551	167791524	0,5	-0,613232941	1
SP42	T12	SP42T12 TRUE	6	168298875	170892848	0,957773469	-0,57645785	
SP42	T12	SP42T12 FALSE	7	286402	54621692	0,621	0,638934588	3
SP42	T12	SP42T12 TRUE	7	54724286	55780176	0,954	3,454117017	36
SP42	T12	SP42T12 FALSE	7	55832454	159025180	0,62	0,603509355	3
SP42	T11	SP42T11 TRUE	8	280241	145750138	0,5	-0,503046869	1
SP42	T10	SP42T10 TRUE	9	286593	20946952	0,961	-0,553352428	2
SP42	T10	SP42T10 TRUE	9	20948311	21695893	0,5	-3,971614216	0
SP42	T10	SP42T10 TRUE	9	21816637	25678122	0,75	-3,135457898	1
SP42	T11	SP42T11 FALSE	9	27044587	43860959	0,69	-0,009452239	2
SP42	T12	SP42T12 TRUE	9	65973514	68409702	0,519	-0,100945976	2
SP42	T11	SP42T11 FALSE	9	68415386	141008876	0,692	-0,033529732	2
SP42	T10	SP42T10 TRUE	10	323283	30728101	0,958	-0,715755692	2
SP42	T11	SP42T11 TRUE	10	30915590	30978282	0,6135	-0,301450297	2
SP42	T12	SP42T12 TRUE	10	30978377	46221393	0,954061836	-0,698001309	
SP42	T11	SP42T11 TRUE	10	46960084	47416860	0,5	-0,770610796	1
SP42	T10	SP42T10 TRUE	10	47605468	51586514	0,957	-0,704405567	2
SP42	T12	SP42T12 TRUE	10	51620278	51631972	0,522	-0,062667075	2
SP42	T12	SP42T12 TRUE	10	51785694	135381766	0,955211704	-0,661429889	
SP42	T12	SP42T12 TRUE	11	193096	50381417	0,504	0,222107404	2
SP42	T12	SP42T12 TRUE	11	51411914	98436532	0,95528182	-0,659169607	
SP42	T11	SP42T11 TRUE	11	99690286	100061865	0,513	-0,529270259	1

SP42	T12	SP42T10	TRUE	11	100064417	105923564	0,951445625	-0,777909416
SP42	T12	SP42T12	TRUE	11	106408212	106849400	0,556	0,010086936 2
SP42	T10	SP42T10	TRUE	11	106849520	134856661	0,957	-0,65218679 2
SP42	T12	SP42T12	TRUE	12	250239	133732624	0,503	0,164035201 2
SP42	T11	SP42T11	FALSE	13	19042919	115091073	0,541	-0,371132036 1
SP42	T11	SP42T11	TRUE	14	19118237	19585390	0,636	-0,640604604 2
SP42	T10	SP42T10	TRUE	14	20085357	81499624	0,962	-0,579473545 2
SP42	T11	SP42T11	TRUE	14	81574844	81610583	0,5	-0,780521565 1
SP42	T12	SP42T12	TRUE	14	82382741	106993845	0,957483538	-0,586329679
SP42	T10	SP42T10	TRUE	14	107087259	107283160	0,899	-0,538062336 2
SP42	T11	SP42T11	FALSE	15	20170150	48752278	0,6045	-0,120254543 2
SP42	T11	SP42T11	TRUE	15	48755168	48813107	0,935201639	-1,194265443
SP42	T11	SP42T11	FALSE	15	48903126	102359203	0,614	-0,108649129 2
SP42	T11	SP42T11	FALSE	16	109665	33412844	0,618	-0,223415439 2
SP42	T11	SP42T11	TRUE	16	33413927	33424950	0,51	-0,157956576 1
SP42	T11	SP42T11	FALSE	16	46389677	90161852	0,609	-0,201544527 2
SP42	T1	SP42T1	FALSE	17	6188	21206440	0,699	-0,329221791 2 1
SP42	T11	SP42T11	FALSE	17	21207844	22253231	0,551	-0,123381594 1
SP42	T11	SP42T11	FALSE	17	25628820	47243622	0,698	-0,272424939 2
SP42	T12	SP42T12	TRUE	17	47579417	81083419	0,5	0,299105202 2
SP42	T11	SP42T11	FALSE	18	334994	77728221	0,595	-0,316358703 2
SP42	T12	SP42T12	FALSE	19	311708	20857775	0,543	0,057891592 2
SP42	T12	SP42T12	TRUE	19	20874651	24014850	0,7165	0,949243222 5

SP42	T12	SP42T1 TRUE	19	28296408	59074653	0,506	0,06225464	2
SP42	T1 TRUE	SP42T1	20	76962	62904542	0,5	0,138122639	2
SP42	T11	SP42T1 TRUE	21	9825966	11058349	0,6185	0,103366264	2
SP42	T12	SP42T1 TRUE	21	14418486	48078611	0,508	0,108736909	2
SP42	T12	SP42T1 TRUE	22	16157827	50169157	0,5	0,144145591	2
SP42	T12	SP42T1 FALSE	22	50277835	50499967	0,687	0,719138386	4
SP42	T12	SP42T1 TRUE	22	50512617	51207915	0,5	0,182456866	2
SP42	T21	SP42T2 TRUE	1	762273	14507057	0,638	-0,177090696	2
SP42	T22	SP42T2 TRUE	1	15441029	237993724	0,5	0,187471124	2
SP42	T21	SP42T2 TRUE	1	239216186	240307048	0,7845	-0,11397225	3
SP42	T22	SP42T2 TRUE	1	240307380	248813749	0,5	0,104526931	2
SP42	T2 FALSE	SP42T2	2	41720	141130501	0,566	0,14888084	2 1
SP42	T20	SP42T2 FALSE	2	141457962	141625410	0,859	-0,692766964	2
SP42	T22	SP42T2 FALSE	2	142012027	242839614	0,561	0,196397188	3
SP42	T22	SP42T2 TRUE	3	386247	197717569	0,5	0,201124979	2
SP42	T2 TRUE	SP42T2	4	60400	189065435	0,5	0,182364671	2 2
SP42	T22	SP42T2 TRUE	5	163205	180670414	0,5	0,181462649	2
SP42	T22	SP42T2 TRUE	6	335251	57841273	0,5	0,170976985	2
SP42	T20	SP42T2 0 FALSE	6	58776982	58778809	0,648914925	-2,675732443	
SP42	T22	SP42T2 TRUE	6	62442604	65149185	0,533	0,278671661	2
SP42	T20	SP42T2 TRUE	6	65300516	68643897	0,856	-1,108004893	1
SP42	T22	SP42T2 0 TRUE	6	69728452	70071173	0,916173344	-0,609392758	
SP42	T23	SP42T2 TRUE	6	70589630	71011831	0,512	0,586251923	3

SP42	T22	SP42T20	TRUE	6	71137992	116600774	0,911082954	-0,694443696
SP42	T21	SP42T2	TRUE	6	116774264	116783330	0,5	-0,307574977 1
SP42	T22	SP42T20	TRUE	6	116836720	167440128	0,909915951	-0,713255361
SP42	T21	SP42T2	TRUE	6	167440244	167591954	0,508	-0,651923542 1
SP42	T22	SP42T20	TRUE	6	167704944	167772755	0,916882594	-0,597134315
SP42	T21	SP42T2	TRUE	6	167786551	167791524	0,556	-0,576482605 1
SP42	T20	SP42T2	TRUE	6	168298875	170892848	0,9155	-0,558105969 2
SP42	T22	SP42T2	TRUE	7	286402	54621692	0,592	0,487965549 3
SP42	T22	SP42T2	TRUE	7	54724286	55780176	0,9205	2,996332778 28
SP42	T21	SP42T2	TRUE	7	55832454	65228128	0,638	-0,1596465 2
SP42	T22	SP42T2	TRUE	7	65439189	159025180	0,595	0,460289369 3
SP42	T21	SP42T2	TRUE	8	280241	145750138	0,64	-0,179220927 2
SP42	T22	SP42T20	TRUE	9	286593	20946952	0,909710937	-0,716534916
SP42	T20	SP42T2	TRUE	9	20948311	21816758	0,5	-2,902551585 0
SP42	T21	SP42T2	TRUE	9	21838145	141008876	0,646	-0,179188572 2
SP42	T22	SP42T20	FALSE	10	323283	46221393	0,927431761	-0,401321944
SP42	T21	SP42T2	TRUE	10	46960084	47416860	0,505	-0,239817708 1
SP42	T23	SP42T20	TRUE	10	47605468	51586514	0,930874436	-0,331203026
SP42	T22	SP42T2	TRUE	10	51620278	51631972	0,5	-0,002439484 2
SP42	T23	SP42T20	TRUE	10	51785694	135381766	0,931987727	-0,307778798
SP42	T22	SP42T2	TRUE	11	193096	50381417	0,5	0,208677957 2
SP42	T22	SP42T20	TRUE	11	51411914	134856661	0,911385629	-0,689524362
SP42	T21	SP42T2	TRUE	12	250239	133732624	0,647	-0,19438342 2

SP42	T21	SP42T2 TRUE	13	19042919	115091073	0,645	-0,198549091	2
SP42	T21	SP42T2 FALSE	14	19118237	19585390	0,614	-0,897271488	1
SP42	T22	SP42T20 TRUE	14	20085357	106993845	0,911319349	-0,690603038	
SP42	T20	SP42T2 TRUE	14	107087259	107283160	0,822	-0,601238211	2
SP42	T21	SP42T2 TRUE	15	20170150	20173275	0,685	-0,130193167	2
SP42	T22	SP42T2 TRUE	15	20279438	48752278	0,5	0,164716568	2
SP42	T22	SP42T20 TRUE	15	48755168	48813107	0,915483973	-0,621208623	
SP42	T22	SP42T2 TRUE	15	48903126	102359203	0,5	0,158010417	2
SP42	T21	SP42T2 FALSE	16	109665	90161852	0,635	-0,266379039	2
SP42	T2TRUE	SP42T2	17	6188	15811871	0,6465	-0,259619622	2 1
SP42	T21	SP42T2 FALSE	17	16004537	22253231	0,612	-0,158154461	2
SP42	T21	SP42T2 TRUE	17	25628820	47121551	0,645	-0,199587417	2
SP42	T22	SP42T2 TRUE	17	47122492	81083419	0,5	0,178925969	2
SP42	T22	SP42T2 TRUE	18	334994	77728221	0,502	0,105030788	2
SP42	T22	SP42T2 TRUE	19	311708	24014850	0,5	-0,022870138	2
SP42	T21	SP42T2 FALSE	19	28296408	59074653	0,575	-0,119974083	2
SP42	T2TRUE	SP42T2	20	76962	26063560	0,508	0,184500007	2 2
SP42	T21	SP42T2 TRUE	20	29449501	29625724	0,722	0,264714655	3
SP42	T22	SP42T2 TRUE	20	29625788	62904542	0,5	0,156684522	2
SP42	T21	SP42T2 FALSE	21	9825966	11058349	0,6185	-0,090712069	2
SP42	T22	SP42T2 TRUE	21	14418486	48078611	0,5	0,136565577	2
SP42	T21	SP42T2 FALSE	22	16157827	49937236	0,631	-0,224195753	2
SP42	T21	SP42T2 FALSE	22	50169157	50354819	0,761	0,434530902	4

SP42	T21	SP42T2 FALSE	22	50470516	51207915	0,625	-0,168823576	2
SP42	T31	SP42T3 TRUE	1	762273	12835868	0,625	-0,204744955	2
SP42	T32	SP42T3 TRUE	1	13182899	248813749	0,503	0,157547168	2
SP42	T3 TRUE	SP42T3	2	41720	141130501	0,5	0,102673436	2 2
SP42	T31	SP42T3 FALSE	2	141457962	141625410	0,7295	-0,130358669	3
SP42	T32	SP42T3 TRUE	2	142012027	242839614	0,5	0,167277901	2
SP42	T32	SP42T3 FALSE	3	386247	197717569	0,573	0,384719595	3
SP42	T3 TRUE	SP42T3	4	60400	189065435	0,5	0,164428641	2 2
SP42	T32	SP42T3 TRUE	5	163205	180670414	0,5	0,159032072	2
SP42	T32	SP42T3 TRUE	6	335251	32548214	0,5	0,091070492	2
SP42	T32	SP42T3 FALSE	6	32548470	32800224	0,621	0,264052196	3
SP42	T32	SP42T3 TRUE	6	32805307	58778809	0,5	0,139981917	2
SP42	T31	SP42T3 TRUE	6	62442604	65622662	0,598	-0,149352793	2
SP42	T30	SP42T3 TRUE	6	65655883	70071173	0,827	-0,56440545	2
SP42	T32	SP42T3 TRUE	6	70589630	71011831	0,586	0,528165161	3
SP42	T30	SP42T3 TRUE	6	71137992	116600774	0,844	-0,597516634	2
SP42	T31	SP42T3 TRUE	6	116774264	116783330	0,538	-0,208420729	1
SP42	T30	SP42T3 TRUE	6	116836720	170892848	0,848	-0,564997176	2
SP42	T32	SP42T3 FALSE	7	286402	54621692	0,6	0,447714215	3
SP42	T32	SP42T3 TRUE	7	54724286	55780176	0,969	4,008742547	68
SP42	T32	SP42T3 FALSE	7	55832454	159025180	0,599	0,38960563	3
SP42	T31	SP42T3 FALSE	8	280241	145750138	0,603	-0,130391226	2
SP42	T30	SP42T3 TRUE	9	286593	20923618	0,84	-0,578467646	2

SP42	T31	SP42T3	9	20946952	141008876	0,606	-0,125262761	2 FALSE
SP42	T33	SP42T3	10	323283	30728101	0,86939122	-0,322920745	0 FALSE
SP42	T31	SP42T3	10	30915590	30978377	0,625	0,023509247	2 TRUE
SP42	T30	SP42T3	10	30978433	46221393	0,87	-0,330698794	3 FALSE
SP42	T31	SP42T3	10	46960084	47416860	0,5	-0,269936302	1 TRUE
SP42	T30	SP42T3	10	47605468	51586514	0,876	-0,197425052	3 TRUE
SP42	T32	SP42T3	10	51620278	51631972	0,513	0,278536089	2 TRUE
SP42	T30	SP42T3	10	51785694	135381766	0,8805	-0,209907633	3 TRUE
SP42	T32	SP42T3	11	193096	50381417	0,5	0,189030065	2 TRUE
SP42	T32	SP42T3	11	51411914	134856661	0,843955582	-0,579625607	0 TRUE
SP42	T31	SP42T3	12	250239	133732624	0,597	-0,111571477	2 FALSE
SP42	T31	SP42T3	13	19042919	115091073	0,602	-0,136183393	2 FALSE
SP42	T30	SP42T3	14	19118237	20085357	0,6355	-0,830429792	1 FALSE
SP42	T32	SP42T3	14	20137084	107283160	0,84280016	-0,590268603	0 TRUE
SP42	T31	SP42T3	15	20170150	20173275	0,508	-0,332423819	1 TRUE
SP42	T32	SP42T3	15	20279438	48752278	0,5	0,136831504	2 TRUE
SP42	T30	SP42T3	15	48755168	48813107	0,846	-0,35797611	2 TRUE
SP42	T32	SP42T3	15	48903126	102359203	0,504	0,099861178	2 TRUE
SP42	T31	SP42T3	16	109665	90161852	0,576	-0,231654672	2 FALSE
SP42	T3TRUE	SP42T3	17	6188	47579417	0,627	-0,24148955	2 1
SP42	T32	SP42T3	17	47696070	81083419	0,5	0,096178725	2 TRUE
SP42	T32	SP42T3	18	334994	77728221	0,506	0,058449045	2 TRUE
SP42	T32	SP42T3	19	311708	59074653	0,5	-0,140870367	2 TRUE

SP42	T3	SP42T3	20	76962	26063560	0,508	0,160489323	2
	TRUE							
SP42	T3	SP42T3	20	29449501	62904542	0,502	0,101144692	2
	2	TRUE						
SP42	T3	SP42T3	21	9825966	15460891	0,626	-0,172918185	2
	1	TRUE						
SP42	T3	SP42T3	21	15481234	48078611	0,505	0,142456304	2
	2	TRUE						
SP42	T3	SP42T3	22	16157827	16953727	0,75	-0,911041512	1
	0	TRUE						
SP42	T3	SP42T3	22	17055458	50169157	0,597	-0,152150768	2
	1	FALSE						
SP42	T3	SP42T3	22	50277835	50499967	0,73	0,347312101	3
	1	FALSE						
SP42	T3	SP42T3	22	50512617	51207915	0,593	-0,069781243	2
	1	FALSE						
SP42	T4	SP42T4	1	762273	12318079	0,57	-0,114172061	2
	1	FALSE						
SP42	T4	SP42T4	1	12339619	248813749	0,5	0,107346803	2
	2	TRUE						
SP42	T4	SP42T4	2	41720	242839614	0,5	0,088636249	2
	TRUE							
SP42	T4	SP42T4	3	386247	197717569	0,5	0,112728386	2
	2	TRUE						
SP42	T4	SP42T4	4	60400	189065435	0,5	0,107341335	2
	TRUE							
SP42	T4	SP42T4	5	163205	180670414	0,5	0,09953025	2
	2	TRUE						
SP42	T4	SP42T4	6	335251	57467323	0,5	0,107917063	2
	2	TRUE						
SP42	T4	SP42T4	6	57841273	70071173	0,631	-0,523167606	1
	0	TRUE						
SP42	T4	SP42T4	6	70589630	71011831	0,5	0,332845264	3
	3	TRUE						
SP42	T4	SP42T4	6	71137992	170892848	0,703	-0,379567363	2
	0	TRUE						
SP42	T4	SP42T4	7	286402	54621692	0,583	0,355800646	3
	2	FALSE						
SP42	T4	SP42T4	7	54724286	55780176	0,7965	2,327357802	24
	5	TRUE						
SP42	T4	SP42T4	7	55832454	159025180	0,584	0,328851688	3
	2	FALSE						
SP42	T4	SP42T4	8	280241	145750138	0,508	-0,033530632	2
	2	TRUE						
SP42	T4	SP42T4	9	286593	20923618	0,7	-0,417940901	2
	0	TRUE						

SP42	T41	SP42T40	9	20946952	141008876	0,566	-0,110946165	2 FALSE
SP42	T42	SP42T40	10	323283	46221393	0,728905051	-0,266169139	FALSE
SP42	T41	SP42T40	10	46960084	47673801	0,519	-0,249136452	1 TRUE
SP42	T40	SP42T40	10	47673858	51586514	0,7335	-0,217158052	3 FALSE
SP42	T42	SP42T40	10	51620278	51631972	0,514	0,086096259	2 TRUE
SP42	T40	SP42T40	10	51785694	135381766	0,737	-0,230034988	3 FALSE
SP42	T42	SP42T40	11	193096	51412353	0,5	0,123806117	2 TRUE
SP42	T40	SP42T40	11	51426207	134856661	0,703	-0,378964202	2 TRUE
SP42	T42	SP42T40	12	250239	133732624	0,505	-0,032130779	2 TRUE
SP42	T41	SP42T40	13	19042919	115091073	0,558	-0,13016898	2 FALSE
SP42	T40	SP42T40	14	19118237	107283160	0,706	-0,391132839	2 TRUE
SP42	T42	SP42T40	15	20170150	48752278	0,5	0,088403961	2 TRUE
SP42	T43	SP42T40	15	48755168	48779402	0,734507279	-0,236043211	TRUE
SP42	T42	SP42T40	15	48797124	102359203	0,5	0,100705068	2 TRUE
SP42	T41	SP42T40	16	109665	33424950	0,5	-0,167426105	1 TRUE
SP42	T40	SP42T40	16	46389677	46394622	0,5	-3,46776357	0 TRUE
SP42	T41	SP42T40	16	46405156	90161852	0,5	-0,129666001	1 TRUE
SP42	T4	SP42T40	17	6188	47579417	0,559	-0,129327629	2 1 FALSE
SP42	T42	SP42T40	17	47696070	81083419	0,5	0,078965485	2 TRUE
SP42	T42	SP42T40	18	334994	77728221	0,5	0,089117772	2 TRUE
SP42	T42	SP42T40	19	311708	59074653	0,503	-0,045819552	2 TRUE
SP42	T4	SP42T40	20	76962	62904542	0,5	0,081379355	2 2 TRUE
SP42	T40	SP42T40	21	9825966	9907416	0,7145	-0,207716499	2 TRUE

SP42	T42	SP42T4 TRUE	21	10971892	14916496	0,52	0,138804678	2
SP42	T41	SP42T40 TRUE	21	15281913	15281957	0,608519889	-0,796309919	
SP42	T42	SP42T4 TRUE	21	15460877	48078611	0,5	0,086504932	2
SP42	T40	SP42T4 TRUE	22	16157827	17055458	0,705	-0,157673867	2
SP42	T42	SP42T4 TRUE	22	17060166	48942566	0,5	-0,110135953	2
SP42	T41	SP42T4 TRUE	22	49246450	50470516	0,659	0,157773254	3
SP42	T41	SP42T4 TRUE	22	50499967	51207915	0,5	-0,142552239	1
SP49	M1	SP49M TRUE	1	865628	248814052	0,5	-0,012181383	1
SP49	M1	SP49M TRUE	2	675831	242794191	0,5	0,002754186	1
SP49	M1	SP49M TRUE	3	386247	197581147	0,504	0,005361827	1
SP49	M TRUE	SP49M	4	64892	189065441	0,5	0,030638571	1 1
SP49	M1	SP49M TRUE	5	163205	179498595	0,5	-0,001003828	1
SP49	M0	SP49M TRUE	5	179528999	179529004	0,762	-0,010722704	1
SP49	M1	SP49M TRUE	5	179529124	180660723	0,5	0,008633197	1
SP49	M1	SP49M TRUE	6	335251	29913344	0,5	-0,055885549	1
SP49	M0	SP49M FALSE	6	29921064	29921242	0,783	-0,689987728	1
SP49	M1	SP49M TRUE	6	29924996	32557483	0,503	-0,003317697	1
SP49	M0	SP49M FALSE	6	32557506	32605451	0,731	-0,238361988	1
SP49	M1	SP49M TRUE	6	32609015	170878886	0,5	-0,037639573	1
SP49	M1	SP49M TRUE	7	331427	159024638	0,5	0,069692724	1
SP49	M1	SP49M TRUE	8	182934	146171437	0,5	-0,011912723	1
SP49	M1	SP49M TRUE	9	214706	141069978	0,5	-0,045466212	1
SP49	M TRUE	SP49M	10	93945	135272948	0,5	-0,077329084	1 1

SP49	M1	SP49M TRUE	11	193865	134238518	0,502	-0,0036868	1
SP49	M1	SP49M TRUE	12	176139	57535266	0,5	-0,039782753	1
SP49	M1	SP49M TRUE	12	57573329	62864417	0,7415	0,654348028	3
SP49	M1	SP49M TRUE	12	62887608	133795960	0,5	-0,001533191	1
SP49	M1	SP49M TRUE	13	19526019	115047700	0,5	0,006545451	1
SP49	M1	SP49M TRUE	14	19188622	107283076	0,5	-0,03890771	1
SP49	M1	SP49M FALSE	15	20170150	20467994	0,644	-0,000358767	1
SP49	M1	SP49M TRUE	15	20588458	102313869	0,5	-0,057765485	1
SP49	M1	SP49M TRUE	16	105325	90142087	0,5	0,002167003	1
SP49	M1	SP49M TRUE	17	177359	81052407	0,505	-0,00482082	1
SP49	M TRUE	SP49M	18	48228	77918221	0,505	-0,00934461	1 1
SP49	M1	SP49M TRUE	19	288062	59082605	0,5	-0,006407524	1
SP49	M TRUE	SP49M	20	76962	62904542	0,5	-0,004176817	1 1
SP49	M1	SP49M TRUE	21	9891930	48083526	0,5	0,056330087	1
SP49	M1	SP49M TRUE	22	16348231	51219006	0,5	-0,061134433	1
SP49	SVZ2	SP49SVZ TRUE	1	865628	59465849	0,5	0,146460773	2
SP49	SVZ0	SP49SVZ TRUE	1	59465881	59465926	0,75	-0,323671964	2
SP49	SVZ2	SP49SVZ TRUE	1	60019782	248814052	0,503	0,143982336	2
SP49	SVZ2	SP49SVZ TRUE	2	675831	136479641	0,509	0,13537146	2
SP49	SVZ1	SP49SVZ FALSE	2	136561557	242794191	0,6	0,009491617	2
SP49	SVZ1	SP49SVZ FALSE	3	386247	174814920	0,533	-0,44153805	1
SP49	SVZ1	SP49SVZ TRUE	3	174974177	186358768	0,9395	2,442604524	25
SP49	SVZ1	SP49SVZ TRUE	3	186360409	191107445	0,8765	1,447103906	12

SP49	SVZ1	SP49SVZ1TRUE	3	192125768	197581147	0,506	-0,417208076	1
SP49	SVZ2	SP49SVZ2TRUE	4	64892	189065441	0,5	0,140694867	2
SP49	SVZ1	SP49SVZ1TRUE	5	163205	180660723	0,5	0,175484722	2
SP49	SVZ1	SP49SVZ1TRUE	6	335251	32261771	0,609	-0,13756386	2
SP49	SVZ1	SP49SVZ1FALSE	6	32268501	32609015	0,644	-0,083434449	2
SP49	SVZ1	SP49SVZ1TRUE	6	32609057	32634467	0,5	-0,265637373	1
SP49	SVZ1	SP49SVZ1TRUE	6	32634482	170878886	0,61	-0,149918271	2
SP49	SVZ2	SP49SVZ2TRUE	7	331427	75183403	0,635	0,590648057	4
SP49	SVZ2	SP49SVZ2TRUE	7	75185985	159024638	0,5795	0,379555951	3
SP49	SVZ2	SP49SVZ20TRUE	8	182934	6794114	0,775299027	-0,543687958	
SP49	SVZ1	SP49SVZ1TRUE	8	7215484	7720995	0,579	-0,694236253	1
SP49	SVZ2	SP49SVZ20TRUE	8	8176221	146171437	0,782442718	-0,497076892	
SP49	SVZ2	SP49SVZ2TRUE	9	214706	131586913	0,5	0,150464311	2
SP49	SVZ2	SP49SVZ2TRUE	9	131670457	141069978	0,582	0,432509352	3
SP49	SVZ2	SP49SVZ2TRUE	10	93945	30728250	0,778	-0,536470069	2
SP49	SVZ1	SP49SVZ1TRUE	10	30915590	30915906	0,512	-0,746660931	1
SP49	SVZ0	SP49SVZ0TRUE	10	30960568	114496687	0,783	-0,499947129	2
SP49	SVZ0	SP49SVZ0FALSE	10	115334124	135272948	0,853	0,095981242	4
SP49	SVZ1	SP49SVZ1TRUE	11	193865	134238518	0,61	-0,131245408	2
SP49	SVZ2	SP49SVZ2TRUE	12	176139	34175508	0,5	0,155692133	2
SP49	SVZ0	SP49SVZ0FALSE	12	37969194	48142418	0,774	-0,489450586	2
SP49	SVZ2	SP49SVZ20TRUE	12	48144243	57592909	0,78523443	-0,478444311	
SP49	SVZ1	SP49SVZ1TRUE	12	57627717	62864417	0,9265	2,056447039	19

SP49	SVZ2	SP49SVZTRUE	12	62887608	133795960	0,5	0,151740824	2
SP49	SVZ1	SP49SVZTRUE	13	19526019	115047700	0,612	-0,162015693	2
SP49	SVZ1	SP49SVZTRUE	14	19188622	107283076	0,607	-0,142336331	2
SP49	SVZ1	SP49SVZTRUE	15	20170150	102313869	0,611	-0,155421629	2
SP49	SVZ2	SP49SVZTRUE	16	105325	90142087	0,5	0,172848424	2
SP49	SVZ0	SP49SVZTRUE	17	177359	18284262	0,83	-0,131266134	3
SP49	SVZ1	SP49SVZTRUE	17	18301096	18314964	0,533	-0,215669905	1
SP49	SVZ0	SP49SVZFALSE	17	18417838	19959693	0,818	-0,094597562	3
SP49	SVZ1	SP49SVZTRUE	17	20000131	81052407	0,614	-0,119104594	2
SP49	SVZTRUE	SP49SVZ	18	48228	77918221	0,5	0,11598802	2 2
SP49	SVZ2	SP49SVZTRUE	19	288062	59082605	0,5	0,151046541	2
SP49	SVZTRUE	SP49SVZ	20	76962	62904542	0,611	-0,119728564	2 1
SP49	SVZ2	SP49SVZTRUE	21	9891930	48083526	0,633	0,546290714	4
SP49	SVZ0	SP49SVZTRUE	22	16348231	51219006	0,785	-0,480021719	2
SP49	T12	SP49T1TRUE	1	865628	58996203	0,503	0,150654012	2
SP49	T11	SP49T1TRUE	1	59096479	59096669	0,698	0,317559645	3
SP49	T12	SP49T1TRUE	1	59096689	248605395	0,504	0,18609838	2
SP49	T11	SP49T1TRUE	1	248722611	248814052	0,6	0,097506759	2
SP49	T12	SP49T1TRUE	2	675831	242794191	0,502	0,137368468	2
SP49	T11	SP49T1FALSE	3	386247	174814920	0,542	-0,346704311	1
SP49	T11	SP49T1TRUE	3	174974177	186395572	0,948	2,587794508	27
SP49	T11	SP49T1TRUE	3	186501502	191107445	0,899	1,795469361	14
SP49	T11	SP49T1FALSE	3	192125768	197581147	0,552	-0,39520961	1

SP49	T1	SP49T1	4	64892	189065441	0,5	0,171172051	2	2
	TRUE								
SP49	T1	SP49T1	5	163205	108516629	0,5	0,190910856	2	
	2	TRUE							
SP49	T1	SP49T1	5	109110537	180660723	0,571	0,395300428	3	
	2	TRUE							
SP49	T1	SP49T1	6	335251	29911419	0,613	-0,128429402	2	
	1	TRUE							
SP49	T1	SP49T1	6	29911538	29921242	0,692	-0,03886164	3	
	1	TRUE							
SP49	T1	SP49T1	6	29924996	170878886	0,614	-0,131209513	2	
	1	TRUE							
SP49	T1	SP49T1	7	331427	75145495	0,636	0,619267388	4	
	2	TRUE							
SP49	T1	SP49T1	7	75168900	159024638	0,584	0,397416822	3	
	2	TRUE							
SP49	T1	SP49T1	8	182934	146171437	0,791	-0,502055045	2	
	0	TRUE							
SP49	T1	SP49T1	9	214706	130446493	0,507	0,19059556	2	
	2	TRUE							
SP49	T1	SP49T1	9	130446836	141069978	0,593	0,437103148	3	
	2	FALSE							
SP49	T1	SP49T1	10	93945	46148326	0,780426001	-0,577232009	2	
	0	FALSE							
SP49	T1	SP49T1	10	46194651	47729407	0,7125	-0,137882313	2	
	0	FALSE							
SP49	T1	SP49T1	10	48370595	135272948	0,792841755	-0,493258025		
	2	0	TRUE						
SP49	T1	SP49T1	11	193865	134238518	0,615	-0,103586667	2	
	1	TRUE							
SP49	T1	SP49T1	12	176139	34175508	0,5	0,158350577	2	
	2	TRUE							
SP49	T1	SP49T1	12	37969194	57592909	0,791653666	-0,501508496		
	2	0	TRUE						
SP49	T1	SP49T1	12	57627717	62864417	0,9385	2,2062155	20	
	1	TRUE							
SP49	T1	SP49T1	12	62887608	133795960	0,5	0,155251062	2	
	2	TRUE							
SP49	T1	SP49T1	13	19526019	115047700	0,618	-0,142142201	2	
	1	TRUE							
SP49	T1	SP49T1	14	19188622	107283076	0,613	-0,129449795	2	
	1	TRUE							
SP49	T1	SP49T1	15	20170150	102313869	0,613	-0,130379061	2	
	1	TRUE							
SP49	T1	SP49T1	16	105325	90142087	0,5	0,16400587	2	
	2	TRUE							

SP49	T13	SP49T10	TRUE	17	177359	18284262	0,838239607	-0,136383192
SP49	T11	SP49T11	FALSE	17	18301096	18314964	0,562	-0,036787358 2
SP49	T13	SP49T10	TRUE	17	18417838	19861458	0,835373911	-0,161717762
SP49	T11	SP49T11	TRUE	17	19959693	81052407	0,614	-0,13660086 2
SP49	T1	SP49T11	TRUE	18	48228	77918221	0,5025	0,151682967 2 2
SP49	T12	SP49T11	TRUE	19	288062	59082605	0,5	0,088560109 2
SP49	T1	SP49T11	TRUE	20	76962	62904542	0,614	-0,1136852 2 1
SP49	T12	SP49T11	TRUE	21	9891930	48083526	0,635	0,572212936 4
SP49	T12	SP49T10	TRUE	22	16348231	51219006	0,793764989	-0,486814052
SP49	T22	SP49T21	TRUE	1	865628	58996203	0,5	0,131090992 2
SP49	T21	SP49T21	TRUE	1	59096479	59096689	0,714	0,249800567 4
SP49	T22	SP49T21	TRUE	1	59096693	248814052	0,503	0,137790008 2
SP49	T22	SP49T21	TRUE	2	675831	242794191	0,5	0,107970011 2
SP49	T21	SP49T21	TRUE	3	386247	174814920	0,5	-0,236668762 1
SP49	T21	SP49T21	TRUE	3	174974177	179689173	0,873	1,525401307 15
SP49	T21	SP49T21	TRUE	3	180630565	186395113	0,929	2,356762342 30
SP49	T21	SP49T21	TRUE	3	186395572	191107445	0,8485	1,363430321 13
SP49	T21	SP49T21	TRUE	3	192125768	197581147	0,5	-0,336844544 1
SP49	T2	SP49T21	TRUE	4	64892	189065441	0,5	0,116517325 2 2
SP49	T22	SP49T21	TRUE	5	163205	180660723	0,5	0,144881016 2
SP49	T21	SP49T21	TRUE	6	335251	170878886	0,583	-0,092165701 2
SP49	T22	SP49T21	TRUE	7	331427	76949920	0,612	0,479768388 4
SP49	T22	SP49T21	TRUE	7	76950686	159024638	0,556	0,28123158 3

SP49	T20	SP49T20TRUE	8	182934	146171437	0,6945	-0,344832779	2
SP49	T22	SP49T22TRUE	9	214706	43875942	0,5	0,116758706	2
SP49	T21	SP49T21TRUE	9	65973404	69120693	0,6	-0,05749896	2
SP49	T22	SP49T22TRUE	9	69238268	130341095	0,5	0,146501766	2
SP49	T22	SP49T22TRUE	9	130341253	141069978	0,566	0,374760445	3
SP49	T20	SP49T20TRUE	10	93945	114496687	0,6920005	-0,353156757	2
SP49	T20	SP49T20FALSE	10	115334124	135272948	0,733	-0,082314816	3
SP49	T21	SP49T21TRUE	11	193865	134238518	0,585	-0,028360423	2
SP49	T22	SP49T22TRUE	12	176139	34175508	0,5	0,128040141	2
SP49	T20	SP49T20TRUE	12	37969194	57592909	0,7	-0,298263924	2
SP49	T21	SP49T21TRUE	12	57627717	62864417	0,91	1,84701751	20
SP49	T22	SP49T22TRUE	12	62887608	133795960	0,506	0,106222028	2
SP49	T21	SP49T21TRUE	13	19526019	115047700	0,578	-0,108294829	2
SP49	T21	SP49T21TRUE	14	19188622	107283076	0,582	-0,092337472	2
SP49	T21	SP49T21TRUE	15	20170150	102313869	0,579	-0,085063924	2
SP49	T22	SP49T22TRUE	16	105325	90142087	0,5	0,138205603	2
SP49	T23	SP49T230TRUE	17	177359	19959693	0,73784939	-0,120624652	
SP49	T21	SP49T21TRUE	17	20000131	81052407	0,586	-0,061927394	2
SP49	T2TRUE	SP49T218TRUE	18	48228	77918221	0,5	0,10416159	2 2
SP49	T22	SP49T22TRUE	19	288062	59082605	0,5	0,056862079	2
SP49	T2TRUE	SP49T220TRUE	20	76962	62904542	0,59	-0,039149745	2 1
SP49	T22	SP49T22TRUE	21	9891930	48083526	0,611	0,450444094	4
SP49	T20	SP49T20TRUE	22	16348231	23077555	0,681	-0,286916513	2

SP49	T22	SP49T220	22	23089759	51219006	0,700712168	-0,311762373	TRUE
SP49	T32	SP49T32	1	865628	248605395	0,5	0,107839017	2 TRUE
SP49	T31	SP49T31	1	248722611	248814052	0,679	0,203759822	4 TRUE
SP49	T32	SP49T32	2	675831	242794191	0,503	0,103163278	2 TRUE
SP49	T31	SP49T31	3	386247	174814920	0,5	-0,220324305	1 TRUE
SP49	T31	SP49T31	3	174974177	186362643	0,884	1,727738606	19 TRUE
SP49	T31	SP49T31	3	186390627	191107445	0,8075	1,035351803	10 TRUE
SP49	T31	SP49T31	3	192125768	197581147	0,5	-0,214575582	1 TRUE
SP49	T3	SP49T3	4	64892	54011526	0,505	0,163413854	2 2 TRUE
SP49	T32	SP49T32	4	54292004	56840846	0,681	0,918854009	7 FALSE
SP49	T32	SP49T32	4	56874517	189065441	0,505	0,109435743	2 TRUE
SP49	T32	SP49T32	5	163205	180660723	0,5	0,15153347	2 TRUE
SP49	T31	SP49T31	6	335251	29855706	0,565	-0,089029169	2 TRUE
SP49	T32	SP49T320	6	29855849	29856092	0,686239895	-0,257620431	FALSE
SP49	T31	SP49T31	6	29856633	29912517	0,559	0,001431976	2 TRUE
SP49	T30	SP49T30	6	29912668	29921242	0,667	-0,137868173	2 TRUE
SP49	T31	SP49T31	6	29924996	170878886	0,571	-0,064365094	2 TRUE
SP49	T32	SP49T32	7	331427	75044830	0,605	0,45136754	4 TRUE
SP49	T32	SP49T32	7	75145495	159024638	0,558	0,29118523	3 TRUE
SP49	T30	SP49T30	8	182934	146171437	0,657	-0,264643001	2 FALSE
SP49	T32	SP49T32	9	214706	43875942	0,503	0,11423469	2 TRUE
SP49	T31	SP49T31	9	65973404	69777287	0,607	0,017760411	3 TRUE
SP49	T32	SP49T32	9	69846339	132377900	0,5	0,124843661	2 TRUE

SP49	T32	SP49T3 FALSE	9	132381749	141069978	0,5325	0,252006285	3
SP49	T30	SP49T3 TRUE	10	93945	114427981	0,66819873	-0,338277916	2
SP49	T30	SP49T3 FALSE	10	114496687	135272948	0,7465	0,055877687	4
SP49	T31	SP49T3 TRUE	11	193865	134238518	0,57	-0,040945184	2
SP49	T32	SP49T3 TRUE	12	176139	34175508	0,5	0,104705285	2
SP49	T30	SP49T3 TRUE	12	37969194	57592909	0,677	-0,286886426	2
SP49	T30	SP49T3 FALSE	12	57627717	62864417	0,914	1,840807444	21
SP49	T32	SP49T3 TRUE	12	62887608	133795960	0,5	0,070637598	2
SP49	T31	SP49T3 FALSE	13	19526019	115047700	0,558	-0,06939029	2
SP49	T31	SP49T3 TRUE	14	19188622	107283076	0,571	-0,069053916	2
SP49	T31	SP49T3 TRUE	15	20170150	102313869	0,565	-0,115646199	2
SP49	T32	SP49T3 TRUE	16	105325	90142087	0,5	0,086059853	2
SP49	T33	SP49T30 TRUE	17	177359	19861458	0,712893987	-0,129542051	
SP49	T31	SP49T3 TRUE	17	19959693	81052407	0,57	-0,093907298	2
SP49	T3 TRUE	SP49T3	18	48228	77918221	0,503	0,065859221	2 2
SP49	T32	SP49T3 TRUE	19	288062	59082605	0,5	0,006604478	2
SP49	T3 TRUE	SP49T3	20	76962	62904542	0,573	-0,0566987	2 1
SP49	T32	SP49T3 TRUE	21	9891930	48083526	0,6015	0,400523483	4
SP49	T32	SP49T30 TRUE	22	16348231	51219006	0,671812449	-0,322479023	
SP49	T42	SP49T4 TRUE	1	865628	58996203	0,5	0,177529012	2
SP49	T41	SP49T4 TRUE	1	59096479	59096693	0,677	0,430674426	3
SP49	T42	SP49T4 TRUE	1	59125894	248814052	0,5	0,187687974	2
SP49	T42	SP49T4 TRUE	2	675831	242794191	0,5	0,085929778	2

SP49	T41	SP49T41 FALSE	3	386247	47555142	0,516	-0,523252369	1
SP49	T41	SP49T41 TRUE	3	47823549	48754583	0,675	0,097955154	3
SP49	T41	SP49T41 FALSE	3	48845251	174814920	0,522	-0,559376505	1
SP49	T41	SP49T41 TRUE	3	174974177	186390627	0,954	2,680764999	25
SP49	T41	SP49T41 TRUE	3	186395113	191107445	0,906	1,73980423	13
SP49	T41	SP49T41 FALSE	3	192125768	197581147	0,5825	-0,649926563	1
SP49	T4	SP49T4 TRUE	4	64892	189065441	0,508	0,123805669	2 2
SP49	T42	SP49T42 TRUE	5	163205	180660723	0,506	0,187663707	2
SP49	T41	SP49T41 TRUE	6	335251	29913344	0,639	-0,148669335	2
SP49	T40	SP49T40 TRUE	6	29921064	29921242	0,862	-0,335089422	2
SP49	T41	SP49T41 TRUE	6	29924996	32331998	0,626	-0,118769456	2
SP49	T41	SP49T41 FALSE	6	32332996	32333439	0,782	-0,001478187	3
SP49	T41	SP49T41 TRUE	6	32333542	32551948	0,657	-0,195191946	2
SP49	T41	SP49T41 FALSE	6	32552029	32628751	0,579	-0,107176129	2
SP49	T41	SP49T41 TRUE	6	32628764	170878886	0,637	-0,179141874	2
SP49	T42	SP49T42 TRUE	7	331427	75044830	0,659	0,732012322	4
SP49	T42	SP49T42 TRUE	7	75145495	159024638	0,58	0,420454278	3
SP49	T42	SP49T420 TRUE	8	182934	7215484	0,860301951	-0,682960174	
SP49	T41	SP49T41 FALSE	8	7277060	7720995	0,6085	-0,900163156	1
SP49	T42	SP49T420 TRUE	8	8176221	11891805	0,871160692	-0,566221122	
SP49	T41	SP49T41 TRUE	8	11990314	12426158	0,571	-0,961706494	1
SP49	T42	SP49T420 TRUE	8	12483982	146171437	0,865666156	-0,626471124	
SP49	T42	SP49T42 TRUE	9	214706	131568363	0,5	0,187086572	2

SP49	T42	SP49T4 TRUE	9	131586913	141069978	0,594	0,506194674	3
SP49	T40	SP49T4 TRUE	10	93945	46194652	0,862690651	-0,65807816	2
SP49	T41	SP49T4 TRUE	10	46963951	46999863	0,643	-0,564064447	2
SP49	T42	SP49T40 TRUE	10	47605468	114496687	0,864860913	-0,635093318	
SP49	T40	SP49T4 TRUE	10	115334124	135272948	0,927	0,240329425	4
SP49	T41	SP49T4 TRUE	11	193865	134238518	0,636	-0,133829258	2
SP49	T42	SP49T4 TRUE	12	176139	34175508	0,5	0,200569694	2
SP49	T40	SP49T4 TRUE	12	37969194	62864417	0,8745	-0,511352243	2
SP49	T42	SP49T4 TRUE	12	62887608	133795960	0,5	0,152604749	2
SP49	T41	SP49T4 TRUE	13	19526019	115047700	0,639	-0,224629444	2
SP49	T41	SP49T4 TRUE	14	19188622	107283076	0,635	-0,168462138	2
SP49	T41	SP49T4 TRUE	15	20170150	102313869	0,636	-0,200492054	2
SP49	T42	SP49T4 TRUE	16	105325	90142087	0,5	0,200537077	2
SP49	T40	SP49T4 TRUE	17	177359	2930339	0,9035	-0,149899485	3
SP49	T41	SP49T4 TRUE	17	2930438	2966308	0,528	-0,1887451	1
SP49	T43	SP49T40 TRUE	17	3019790	18284262	0,900963073	-0,186686758	
SP49	T41	SP49T4 FALSE	17	18301096	18314964	0,611	0,049395543	2
SP49	T43	SP49T40 TRUE	17	18417838	19959693	0,901851206	-0,173690741	
SP49	T41	SP49T4 TRUE	17	20000131	81052407	0,635	-0,148564795	2
SP49	T4 TRUE	SP49T4	18	48228	77918221	0,5	0,174476401	2 2
SP49	T42	SP49T4 TRUE	19	288062	59082605	0,5	0,137301863	2
SP49	T4 TRUE	SP49T4	20	76962	62904542	0,638	-0,110127838	2 1
SP49	T42	SP49T4 TRUE	21	9891930	48083526	0,648	0,653045192	4

SP49	T40	SP49T40 TRUE	22	16348231	16436533	0,7035	-0,642386092	1
SP49	T40	SP49T40 TRUE	22	16906273	45622351	0,871	-0,586246177	2
SP49	T41	SP49T41 TRUE	22	45723960	45724214	0,6	-0,438151075	2
SP49	T42	SP49T40 TRUE	22	45897997	51219006	0,873316224	-0,541880078	
SP52	M1	SP52M1 TRUE	1	878253	249110906	0,502	-0,006717529	1
SP52	M1	SP52M1 TRUE	2	224970	242758203	0,5	0,01246444	1
SP52	M1	SP52M1 TRUE	2	242758326	242758475	0,737	-0,539949857	1
SP52	M1	SP52M1 TRUE	3	361508	197581147	0,504	-0,002570191	1
SP52	M TRUE	SP52M	4	49846	190328957	0,5	0,024761693	1
SP52	M1	SP52M1 TRUE	5	163205	180687212	0,505	0,003344715	1
SP52	M1	SP52M1 TRUE	6	335251	29704259	0,503	-0,009514313	1
SP52	M1	SP52M1 FALSE	6	29709402	29768917	0,615	-0,091498432	1
SP52	M1	SP52M1 TRUE	6	29768957	29897061	0,507	0,102291943	1
SP52	M1	SP52M1 TRUE	6	29897301	29910866	0,632	0,052413908	2
SP52	M1	SP52M1 TRUE	6	29911011	170892848	0,5	0,031407125	1
SP52	M1	SP52M1 TRUE	7	330104	159053596	0,5	-0,012457853	1
SP52	M1	SP52M1 TRUE	8	182934	146220940	0,5	0,019205256	1
SP52	M1	SP52M1 TRUE	9	117713	141071552	0,5	0,001378552	1
SP52	M1	SP52M1 TRUE	10	132135	135197419	0,5	-0,004058041	1
SP52	M1	SP52M1 TRUE	11	193096	134252121	0,5	0,015802146	1
SP52	M1	SP52M1 TRUE	12	247900	133808275	0,5	0,000596005	1
SP52	M1	SP52M1 TRUE	13	19241342	115064542	0,5	0,023887144	1
SP52	M1	SP52M1 TRUE	14	19114712	107137063	0,506	-0,003301581	1

SP52	M1	SP52M TRUE	14	107156824	107169755	0,823	0,439491959	2
SP52	M1	SP52M TRUE	15	20086442	102304770	0,5	-0,013936584	1
SP52	M TRUE	SP52M	16	81639	90109711	0,505	-0,060417918	1 1
SP52	M TRUE	SP52M	17	6115	81006629	0,5	-0,040830849	1 1
SP52	M TRUE	SP52M	18	12893	77893683	0,506	0,031120645	1 1
SP52	M1	SP52M TRUE	19	291184	58991638	0,5	-0,084632586	1
SP52	M1	SP52M TRUE	20	168781	62904542	0,504	-0,013625537	1
SP52	M0	SP52M FALSE	21	9912042	9912117	0,796	-0,313253932	1
SP52	M1	SP52M TRUE	21	10793702	48083526	0,5	-0,025521962	1
SP52	M1	SP52M TRUE	22	16348231	51211392	0,505	-0,054248811	1
SP52	SVZ1	SP52SVZ TRUE	1	878253	16976679	0,5	-0,094572857	1
SP52	SVZ1	SP52SVZ 0 TRUE	1	17026087	17083685	0,587842377	-0,218810497	
SP52	SVZ1	SP52SVZ TRUE	1	17083872	249110906	0,505	0,007334007	1
SP52	SVZ1	SP52SVZ TRUE	2	224970	242758475	0,5	0,010018141	1
SP52	SVZ1	SP52SVZ TRUE	3	361508	192874117	0,504	0,010609071	1
SP52	SVZ1	SP52SVZ 0 FALSE	3	193016895	197581147	0,576859879	-0,256749802	
SP52	SVZ TRUE	SP52SVZ	4	49846	190328957	0,5	0,034267136	1 1
SP52	SVZ1	SP52SVZ TRUE	5	163205	180687212	0,5	0,000433078	1
SP52	SVZ1	SP52SVZ FALSE	6	335251	29704259	0,51	0,011897635	1
SP52	SVZ0	SP52SVZ TRUE	6	29709402	29709665	0,6465	0,191625944	2
SP52	SVZ1	SP52SVZ TRUE	6	29712878	170892848	0,5	0,037775974	1
SP52	SVZ1	SP52SVZ FALSE	7	330104	159053596	0,554	0,18709868	2
SP52	SVZ1	SP52SVZ TRUE	8	182934	146220940	0,5	0,007068582	1

SP52	SVZ0	SP52SVZ0 TRUE	9	117713	31254567	0,588	-0,205570489	1
SP52	SVZ1	SP52SVZ1 TRUE	9	32333630	132863158	0,503	-0,000821327	1
SP52	SVZ1	SP52SVZ0 TRUE	9	132891113	139091797	0,576168874	-0,259103861	
SP52	SVZ1	SP52SVZ1 TRUE	9	139142808	141071552	0,511	-0,040094533	1
SP52	SVZ0	SP52SVZ0 TRUE	10	132135	135197419	0,584	-0,232605052	1
SP52	SVZ1	SP52SVZ1 TRUE	11	193096	134252121	0,5	0,011033234	1
SP52	SVZ1	SP52SVZ1 TRUE	12	247900	133808275	0,5	0,017168508	1
SP52	SVZ1	SP52SVZ0 TRUE	13	19241342	107863171	0,590407827	-0,209802464	
SP52	SVZ1	SP52SVZ1 TRUE	13	108861913	111980537	0,922	2,574638735	34
SP52	SVZ0	SP52SVZ0 FALSE	13	112315737	115064542	0,569	-0,22900752	1
SP52	SVZ1	SP52SVZ1 TRUE	14	19114712	107169755	0,505	-0,000357884	1
SP52	SVZ0	SP52SVZ0 TRUE	15	20086442	102304770	0,586	-0,213645969	1
SP52	SVZ TRUE	SP52SVZ TRUE	16	81639	90109711	0,5	-0,039208994	1	1
SP52	SVZ TRUE	SP52SVZ TRUE	17	6115	22066776	0,505	-0,020640928	1	1
SP52	SVZ0	SP52SVZ0 FALSE	17	25352308	39134659	0,5505	-0,10911124	1
SP52	SVZ0	SP52SVZ0 FALSE	17	39135084	39135322	0,533489568	-0,397523662	
SP52	SVZ1	SP52SVZ0 TRUE	17	39137104	40375309	0,589622318	-0,212566591	
SP52	SVZ1	SP52SVZ1 TRUE	17	41046440	81006629	0,5	-0,029419331	1
SP52	SVZ TRUE	SP52SVZ TRUE	18	12893	77893683	0,507	0,026360599	1	1
SP52	SVZ1	SP52SVZ1 TRUE	19	291184	50453317	0,5	-0,049596285	1
SP52	SVZ1	SP52SVZ1 TRUE	19	50455351	58991638	0,5595	0,174699933	2
SP52	SVZ1	SP52SVZ1 TRUE	20	168781	62904542	0,564	0,186518782	2
SP52	SVZ0	SP52SVZ0 TRUE	21	9912042	11181699	0,576	-0,078435857	1

SP52	SVZ1	SP52SVZ1 TRUE	21	14414959	48083526	0,5	-0,021708681	1
SP52	SVZ1	SP52SVZ1 TRUE	22	16348231	51211392	0,5	-0,035898109	1
SP52	T11	SP52T11 TRUE	1	878253	5935162	0,5	0,028955134	1
SP52	T10	SP52T10 TRUE	1	6100458	9416346	0,699	-0,485141708	1
SP52	T11	SP52T11 TRUE	1	9627521	249110906	0,5	-0,016164421	1
SP52	T11	SP52T11 TRUE	2	224970	87106108	0,5	-0,027375841	1
SP52	T10	SP52T10 TRUE	2	88005546	89309762	0,717	-0,339991018	1
SP52	T11	SP52T11 TRUE	2	89319834	91872945	0,5195	-0,375851874	1
SP52	T12	SP52T120 TRUE	2	91873005	91886089	0,778040558	-0,080888997	
SP52	T11	SP52T11 TRUE	2	95527944	242758475	0,504	-0,01023547	1
SP52	T11	SP52T11 TRUE	3	361508	90276661	0,5	-0,022632395	1
SP52	T10	SP52T10 TRUE	3	93593119	97753931	0,696	-0,504530039	1
SP52	T11	SP52T11 TRUE	3	97806616	191107192	0,505	-0,02165992	1
SP52	T10	SP52T10 FALSE	3	192053274	197581147	0,672	-0,515669578	1
SP52	T1 TRUE	SP52T1	4	49846	190328957	0,5	-0,006701493	1 1
SP52	T11	SP52T11 TRUE	5	163205	180687212	0,5	-0,01763196	1
SP52	T11	SP52T11 TRUE	6	335251	29709402	0,504	-0,00051531	1
SP52	T10	SP52T10 FALSE	6	29709445	29709665	0,667	-0,322313682	1
SP52	T11	SP52T11 TRUE	6	29712878	29897061	0,5	0,036425257	1
SP52	T10	SP52T10 FALSE	6	29897301	29910562	0,676	-0,033296304	1
SP52	T11	SP52T11 TRUE	6	29910742	31324615	0,51	0,097180027	1
SP52	T10	SP52T10 FALSE	6	31324702	31324750	0,791	0,607218336	3
SP52	T11	SP52T11 TRUE	6	31324864	170892848	0,5	0,005406043	1

SP52	T11	SP52T1 TRUE	7	330104	73150511	0,615	0,351833521	2
SP52	T11	SP52T1 FALSE	7	73151644	159053596	0,5395	0,155230587	1
SP52	T11	SP52T1 TRUE	8	182934	146220940	0,5	0,000870583	1
SP52	T10	SP52T1 TRUE	9	117713	32334264	0,696	-0,518162539	1
SP52	T11	SP52T1 TRUE	9	32384825	132662786	0,507	-0,028657845	1
SP52	T10	SP52T1 TRUE	9	132845689	138416565	0,699	-0,521825874	1
SP52	T11	SP52T1 TRUE	9	138440525	138662309	0,517	-0,086102527	1
SP52	T10	SP52T1 TRUE	9	138662661	138903671	0,696	-0,438183285	1
SP52	T11	SP52T1 TRUE	9	139008803	141071552	0,507	0,059339806	1
SP52	T10	SP52T1 TRUE	10	132135	46280866	0,697	-0,547696681	1
SP52	T10	SP52T1 TRUE	10	46960084	47087501	0,509	-0,549169379	0
SP52	T10	SP52T1 TRUE	10	47605468	51582894	0,7055	-0,458137726	1
SP52	T10	SP52T1 TRUE	10	51620231	51633027	0,517	-0,812493705	0
SP52	T10	SP52T1 TRUE	10	52086939	135197419	0,7	-0,515245951	1
SP52	T11	SP52T1 TRUE	11	193096	134252121	0,5035	-0,002768155	1
SP52	T11	SP52T1 TRUE	12	247900	133808275	0,508	-0,015419737	1
SP52	T11	SP52T10 TRUE	13	19241342	24384129	0,665250825	-0,673673416	
SP52	T11	SP52T1 TRUE	13	24436475	25029113	0,52	-0,426334998	1
SP52	T11	SP52T10 TRUE	13	25030447	99092179	0,700581867	-0,512754509	
SP52	T10	SP52T1 FALSE	13	99098318	107863171	0,675	-0,499250155	1
SP52	T11	SP52T1 TRUE	13	108861913	111980537	0,958	3,647623548	41
SP52	T10	SP52T1 TRUE	13	112315737	115064542	0,6825	-0,488023451	1
SP52	T11	SP52T1 TRUE	14	19114712	64886426	0,503	-0,01612975	1

SP52	T10	SP52T1 TRUE	14	64894362	64907994	0,656	-0,365583954	1
SP52	T11	SP52T1 TRUE	14	64908651	107169755	0,5	-0,01368599	1
SP52	T11	SP52T1 TRUE	15	20086442	22929906	0,5	-0,231818414	1
SP52	T10	SP52T1 TRUE	15	22933528	102304770	0,7	-0,519464046	1
SP52	T1 TRUE	SP52T1	16	81639	90109711	0,5	-0,030260493	1 1
SP52	T1 TRUE	SP52T1	17	6115	30822034	0,5	-0,024039688	1 1
SP52	T10	SP52T1 FALSE	17	31319033	35783812	0,667	-0,457327413	1
SP52	T11	SP52T1 TRUE	17	35896123	36358847	0,509	-0,057211401	1
SP52	T11	SP52T1 0 TRUE	17	36398000	39969549	0,686022503	-0,581254081	
SP52	T11	SP52T1 FALSE	17	40021498	81006629	0,521	0,190999588	1
SP52	T1 TRUE	SP52T1	18	12893	77893683	0,5	-0,021070015	1 1
SP52	T11	SP52T1 TRUE	19	291184	50475114	0,5	-0,037632949	1
SP52	T11	SP52T1 TRUE	19	50475174	58991638	0,61	0,318349939	2
SP52	T11	SP52T1 TRUE	20	168781	62904542	0,606	0,331273023	2
SP52	T11	SP52T1 TRUE	21	9912042	48083526	0,5	-0,019948224	1
SP52	T11	SP52T1 TRUE	22	16348231	51211392	0,503	-0,020468265	1
SP52	T21	SP52T2 TRUE	1	878253	5935162	0,508	-0,075423556	1
SP52	T21	SP52T2 0 TRUE	1	6100458	9009214	0,772975834	-0,711398262	
SP52	T20	SP52T2 TRUE	1	9009406	9324213	0,5	-1,744394892	0
SP52	T20	SP52T2 FALSE	1	9416346	10708300	0,745	-0,651449246	1
SP52	T21	SP52T2 TRUE	1	11018723	16748432	0,5	-0,095426925	1
SP52	T20	SP52T2 FALSE	1	16767359	17083888	0,63	-0,020109461	1
SP52	T21	SP52T2 TRUE	1	17084006	249110906	0,5	0,003820945	1

SP52	T21	SP52T21 TRUE	2	224970	87106108	0,5	0,013153146	1
SP52	T21	SP52T210 TRUE	2	88005546	89319834	0,799497398	-0,532173345	
SP52	T21	SP52T21 FALSE	2	89339720	91872945	0,522	-0,360464436	1
SP52	T20	SP52T20 TRUE	2	91873005	91873025	0,844	0,157722924	2
SP52	T21	SP52T21 TRUE	2	91885946	242758475	0,5	0,020710123	1
SP52	T21	SP52T21 TRUE	3	361508	97611916	0,5	-0,015273783	1
SP52	T20	SP52T20 TRUE	3	97634253	97753931	0,767	-0,698063076	1
SP52	T21	SP52T21 TRUE	3	97806616	191107192	0,5	0,018952493	1
SP52	T21	SP52T210 TRUE	3	192053274	195395272	0,779434124	-0,669761989	
SP52	T21	SP52T21 FALSE	3	195395328	195453243	0,6105	-0,217465562	1
SP52	T20	SP52T20 TRUE	3	195466972	197581147	0,773	-0,744128779	1
SP52	T2TRUE	SP52T2	4	49846	190328957	0,5	0,035370769	1 1
SP52	T21	SP52T21 TRUE	5	163205	180687212	0,506	0,001607123	1
SP52	T21	SP52T21 TRUE	6	335251	29704259	0,5055	0,004996301	1
SP52	T21	SP52T21 FALSE	6	29709402	29712878	0,671	0,242923746	2
SP52	T21	SP52T21 TRUE	6	29718578	31324615	0,509	0,003035422	1
SP52	T20	SP52T20 TRUE	6	31324702	31324750	0,8	-0,434532034	1
SP52	T21	SP52T21 TRUE	6	31324864	116720487	0,5	0,014897063	1
SP52	T20	SP52T20 TRUE	6	116774259	116774616	0,8305	-0,252143817	2
SP52	T21	SP52T21 TRUE	6	116836720	170892848	0,5	0,036893354	1
SP52	T21	SP52T21 TRUE	7	330104	159053596	0,634	0,447157969	2
SP52	T21	SP52T21 TRUE	8	182934	146220940	0,503	0,011843367	1
SP52	T20	SP52T20 TRUE	9	117713	21441116	0,783	-0,647622525	1

SP52	T20	SP52T20 TRUE	9	21861903	22748135	0,5	-1,881790968	0
SP52	T20	SP52T20 TRUE	9	23705108	31254567	0,793	-0,579655677	1
SP52	T21	SP52T21 TRUE	9	32333630	132662786	0,5	-0,011888769	1
SP52	T21	SP52T21 TRUE	9	132845689	138415238	0,773810869	-0,706081988	
SP52	T21	SP52T21 TRUE	9	138416565	138555161	0,55	-0,201121683	1
SP52	T20	SP52T20 TRUE	9	138662309	138903671	0,785	-0,592769062	1
SP52	T21	SP52T21 TRUE	9	139008803	141071552	0,507	-0,035501813	1
SP52	T21	SP52T21 TRUE	10	132135	19780543	0,777678045	-0,681202808	
SP52	T20	SP52T20 TRUE	10	20506326	20507790	0,5	-1,489271305	0
SP52	T21	SP52T21 TRUE	10	21076100	46280866	0,781521648	-0,656042719	
SP52	T20	SP52T20 TRUE	10	46960084	47087501	0,5	-0,75339897	0
SP52	T21	SP52T21 TRUE	10	47605468	47668747	0,797347589	-0,547559724	
SP52	T20	SP52T20 TRUE	10	47677955	51582894	0,794	-0,588225244	1
SP52	T20	SP52T20 FALSE	10	51620231	51633027	0,594	-0,809955017	0
SP52	T21	SP52T21 TRUE	10	52086939	135197419	0,78053145	-0,662566601	
SP52	T21	SP52T21 TRUE	11	193096	134252121	0,5	-0,012387956	1
SP52	T21	SP52T21 TRUE	12	247900	133808275	0,5	0,014472121	1
SP52	T21	SP52T21 TRUE	13	19241342	107863171	0,788381882	-0,610015538	
SP52	T21	SP52T21 TRUE	13	108861913	111980537	0,967	3,802593217	37
SP52	T20	SP52T20 TRUE	13	112315737	115064542	0,787	-0,566688458	1
SP52	T21	SP52T21 TRUE	14	19114712	107169755	0,5	0,012278492	1
SP52	T21	SP52T21 TRUE	15	20086442	22567365	0,507	-0,197133668	1
SP52	T20	SP52T20 TRUE	15	22777680	34782508	0,783	-0,621621502	1

SP52	T20	SP52T20	15	34848715	34848959	0,554	-0,85096268	0 TRUE
SP52	T21	SP52T20	15	35141453	102304770	0,78138873	-0,656920161	TRUE
SP52	T2 TRUE	SP52T2	16	81639	90109711	0,5	-0,027876045	1 1
SP52	T2 TRUE	SP52T2	17	6115	30822034	0,5	-0,020891445	1 1
SP52	T20	SP52T2	17	31319033	35783812	0,777	-0,617130431	1 FALSE
SP52	T21	SP52T2	17	35896123	36358847	0,508	-0,055099465	1 TRUE
SP52	T21	SP52T20	17	36398000	40375309	0,771052061	-0,723571964	TRUE
SP52	T21	SP52T2	17	41046440	81006629	0,5	-0,032239499	1 TRUE
SP52	T2 TRUE	SP52T2	18	12893	77893683	0,5	0,008280437	1 1
SP52	T21	SP52T2	19	291184	47969394	0,5	-0,051998592	1 TRUE
SP52	T21	SP52T2	19	48182787	48382157	0,695	0,078326012	2 FALSE
SP52	T21	SP52T2	19	48389363	50542359	0,5	-0,075245195	1 TRUE
SP52	T21	SP52T2	19	50562372	58991638	0,636	0,428760239	2 TRUE
SP52	T21	SP52T2	20	168781	26189088	0,627	0,46830051	2 TRUE
SP52	T21	SP52T2	20	29449333	62904542	0,634	0,417107179	2 TRUE
SP52	T21	SP52T2	21	9912042	48083526	0,5	-0,029652392	1 TRUE
SP52	T21	SP52T2	22	16348231	51211392	0,5	-0,037543061	1 TRUE
SP52	T31	SP52T3	1	878253	5935162	0,512	-0,049041638	1 FALSE
SP52	T31	SP52T3	1	6100458	9416346	0,801492444	-0,740052021	0 TRUE
SP52	T31	SP52T3	1	9627521	121116121	0,5	-0,020363917	1 TRUE
SP52	T31	SP52T3	1	142688899	143403644	0,625	0,081040872	2 TRUE
SP52	T31	SP52T3	1	143767643	249110906	0,577	0,242557766	1 FALSE
SP52	T31	SP52T3	2	224970	88327387	0,5	-0,015832158	1 TRUE

SP52	T30	SP52T3 TRUE	2	88748390	89319834	0,814	-0,57237273	1
SP52	T30	SP52T3 FALSE	2	89339720	91886089	0,6235	-0,301945725	1
SP52	T31	SP52T3 TRUE	2	95527944	242758475	0,5	0,014714599	1
SP52	T31	SP52T3 TRUE	3	361508	97611916	0,5065	-0,017940979	1
SP52	T31	SP52T3 TRUE	3	97634253	97753931	0,798512615	-0,761547615	
SP52	T31	SP52T3 TRUE	3	97806616	191107192	0,5	0,009821292	1
SP52	T31	SP52T3 TRUE	3	192053274	195395272	0,80855277	-0,687804886	
SP52	T31	SP52T3 TRUE	3	195395328	195426231	0,517	-0,354136172	1
SP52	T31	SP52T3 TRUE	3	195452805	197581147	0,784511952	-0,858465952	
SP52	T3TRUE	SP52T3	4	49846	190328957	0,5	0,033615673	1
SP52	T31	SP52T3 TRUE	5	163205	180687212	0,5	0,001779807	1
SP52	T31	SP52T3 TRUE	6	335251	170892848	0,5	0,030991648	1
SP52	T31	SP52T3 TRUE	7	330104	159053596	0,637	0,465596401	2
SP52	T31	SP52T3 TRUE	8	182934	146220940	0,503	0,018642433	1
SP52	T31	SP52T3 TRUE	9	117713	21441116	0,806601611	-0,702433877	
SP52	T30	SP52T3 TRUE	9	21861903	22748135	0,52	-2,056169554	0
SP52	T30	SP52T3 TRUE	9	23705108	28863459	0,808	-0,663412839	1
SP52	T31	SP52T3 TRUE	9	31254567	132662786	0,5	-0,026571883	1
SP52	T30	SP52T3 TRUE	9	132845689	138416565	0,8075	-0,722962115	1
SP52	T31	SP52T3 FALSE	9	138440525	138662309	0,524	-0,165849513	1
SP52	T30	SP52T3 TRUE	9	138662661	138903671	0,811	-0,634340089	1
SP52	T31	SP52T3 TRUE	9	139008803	141071552	0,513	-0,034987003	1
SP52	T31	SP52T3 TRUE	10	132135	30739058	0,801567836	-0,739503992	

SP52	T30	SP52T30 TRUE	10	30915590	30978274	0,5	-0,966616749	0
SP52	T31	SP52T30 TRUE	10	30987520	46280866	0,804344788	-0,719171641	
SP52	T31	SP52T30 TRUE	10	46960084	47667164	0,511	-0,663492828	1
SP52	T30	SP52T30 TRUE	10	47668707	51620231	0,8055	-0,684500044	1
SP52	T30	SP52T30 TRUE	10	51623004	51633027	0,531	-0,944833491	0
SP52	T31	SP52T30 TRUE	10	52086939	135197419	0,805572302	-0,710091857	
SP52	T31	SP52T30 TRUE	11	193096	134252121	0,5	-0,008978766	1
SP52	T31	SP52T30 TRUE	12	247900	133808275	0,5	0,002357976	1
SP52	T31	SP52T30 TRUE	13	19241342	24877445	0,792551221	-0,803613266	
SP52	T31	SP52T30 FALSE	13	24895559	24933805	0,619	-0,514882783	1
SP52	T31	SP52T30 TRUE	13	25023936	107863171	0,807512053	-0,695626207	
SP52	T31	SP52T30 TRUE	13	108861913	111980537	0,915	2,610035123	14
SP52	T30	SP52T30 TRUE	13	112315737	115064542	0,799	-0,701521657	1
SP52	T31	SP52T30 TRUE	14	19114712	107169755	0,5	0,008369691	1
SP52	T31	SP52T30 TRUE	15	20086442	22567365	0,517	-0,238307218	1
SP52	T31	SP52T30 TRUE	15	22777680	34782508	0,805849974	-0,708029996	
SP52	T30	SP52T30 TRUE	15	34848715	34848959	0,545	-0,836972844	0
SP52	T31	SP52T30 TRUE	15	35141453	102304770	0,803451563	-0,725742991	
SP52	T3TRUE	SP52T30 TRUE	16	81639	33425202	0,509	-0,062711621	1 1
SP52	T31	SP52T30 FALSE	16	47733115	90109711	0,618	-0,349110584	1
SP52	T3TRUE	SP52T30 TRUE	17	6115	30822034	0,503	-0,013247641	1 1
SP52	T30	SP52T30 FALSE	17	31319033	34432125	0,7815	-0,656970153	1
SP52	T31	SP52T30 TRUE	17	34432297	34952964	0,79535802	-0,783960227	

SP52	T31	SP52T3	17	35306312	36398000	0,511	-0,227144443	1
		TRUE						
SP52	T31	SP52T3	17	36520567	40375309	0,797262932	-0,770467989	
		0 TRUE						
SP52	T31	SP52T3	17	41046440	81006629	0,5	-0,053582612	1
		TRUE						
SP52	T31	SP52T3	18	12893	77893683	0,5	0,014571975	1
	TRUE							
SP52	T31	SP52T3	19	291184	50563208	0,5	-0,080828048	1
		TRUE						
SP52	T31	SP52T3	19	50563239	58991638	0,64	0,385448711	2
		TRUE						
SP52	T31	SP52T3	20	168781	26189088	0,639	0,428148241	2
		TRUE						
SP52	T31	SP52T3	20	29449333	62904542	0,6335	0,412816041	2
		TRUE						
SP52	T31	SP52T3	21	9912042	15386049	0,606	-0,21155079	1
		FALSE						
SP52	T31	SP52T3	21	15593286	48083526	0,5	-0,007000005	1
		TRUE						
SP52	T31	SP52T3	22	16348231	51211392	0,5	-0,047574549	1
		TRUE						
SP52	T41	SP52T4	1	878253	5935162	0,51	-0,041839875	1
		TRUE						
SP52	T41	SP52T4	1	6100458	9416346	0,788252451	-0,774333957	
		0 TRUE						
SP52	T41	SP52T4	1	9627521	121116121	0,5	-0,013061194	1
		TRUE						
SP52	T41	SP52T4	1	142688899	144854454	0,711	0,131199554	2
		FALSE						
SP52	T41	SP52T4	1	144860026	249110906	0,5	0,038034419	1
		TRUE						
SP52	T41	SP52T4	2	224970	88327387	0,5	0,012339127	1
		TRUE						
SP52	T41	SP52T4	2	88748390	89319834	0,810574833	-0,613616707	
		0 TRUE						
SP52	T41	SP52T4	2	89339720	91886089	0,5895	-0,298202165	1
		FALSE						
SP52	T41	SP52T4	2	95527944	242758475	0,506	0,030883979	1
		TRUE						
SP52	T41	SP52T4	3	361508	97611916	0,5	0,010411723	1
		TRUE						
SP52	T40	SP52T4	3	97634253	97753931	0,809	-0,55025327	1
		TRUE						
SP52	T41	SP52T4	3	97806616	191107192	0,5	0,023651043	1
		TRUE						

SP52	T41	SP52T40	TRUE	3	192053274	195395272	0,800107587	-0,691212397
SP52	T41	SP52T40	FALSE	3	195395328	195426231	0,603	-0,183118951 1
SP52	T41	SP52T40	TRUE	3	195452805	197581147	0,777811881	-0,843770358
SP52	T41	SP52T40	TRUE	4	49846	190328957	0,5	0,043915721 1 1
SP52	T41	SP52T40	TRUE	5	163205	180687212	0,5	0,012080726 1
SP52	T41	SP52T40	TRUE	6	335251	29704259	0,5	0,02136229 1
SP52	T41	SP52T40	FALSE	6	29709402	29709602	0,67	0,24593634 2
SP52	T41	SP52T40	FALSE	6	29709610	29975775	0,552	0,040695941 1
SP52	T41	SP52T40	TRUE	6	29976262	170892848	0,5	0,032130746 1
SP52	T41	SP52T40	TRUE	7	330104	159053596	0,638	0,459989635 2
SP52	T41	SP52T40	TRUE	8	182934	146220940	0,5	0,044427994 1
SP52	T41	SP52T40	TRUE	9	117713	21441116	0,80268654	-0,672478059
SP52	T40	SP52T40	TRUE	9	21861903	22748135	0,515	-1,833815647 0
SP52	T41	SP52T40	TRUE	9	23705108	28863459	0,810780257	-0,612051313
SP52	T41	SP52T40	TRUE	9	31254567	66711328	0,503	0,007182257 1
SP52	T41	SP52T40	FALSE	9	68409659	69120693	0,727	0,012077893 2
SP52	T41	SP52T40	TRUE	9	69847032	132662786	0,5	0,017476216 1
SP52	T41	SP52T40	TRUE	9	132845689	138415238	0,795999288	-0,720562874
SP52	T41	SP52T40	TRUE	9	138416565	138555161	0,507	-0,177959263 1
SP52	T41	SP52T40	TRUE	9	138662309	138903671	0,813945569	-0,587713432
SP52	T41	SP52T40	TRUE	9	139008803	141071552	0,504	0,023037478 1
SP52	T41	SP52T40	TRUE	10	132135	30739058	0,794186375	-0,733327181
SP52	T41	SP52T40	TRUE	10	30915590	30978274	0,5	-0,564071808 1

SP52	T41	SP52T40	TRUE	10	30987520	46280866	0,798921331	-0,699748734
SP52	T40	SP52T40	TRUE	10	46960084	47087501	0,515	-0,721704671 0
SP52	T40	SP52T40	TRUE	10	47605468	51582894	0,7965	-0,59541239 1
SP52	T41	SP52T40	TRUE	10	51620231	51633027	0,507	-0,60954375 1
SP52	T41	SP52T40	TRUE	10	52086939	135197419	0,802190877	-0,676097648
SP52	T41	SP52T40	TRUE	11	193096	134252121	0,503	0,015347699 1
SP52	T41	SP52T40	TRUE	12	247900	133808275	0,5	0,018110495 1
SP52	T40	SP52T40	TRUE	13	19241342	107863171	0,807	-0,646002223 1
SP52	T41	SP52T40	TRUE	13	108861913	111980537	0,954	3,453225904 27
SP52	T40	SP52T40	TRUE	13	112315737	115064542	0,8035	-0,600626469 1
SP52	T41	SP52T40	TRUE	14	19114712	107137063	0,503	-0,000285718 1
SP52	T41	SP52T40	FALSE	14	107156824	107169755	0,726	0,289049648 2
SP52	T41	SP52T40	TRUE	15	20086442	22567365	0,5	-0,195002183 1
SP52	T41	SP52T40	TRUE	15	22777680	34782508	0,801773735	-0,679136818
SP52	T40	SP52T40	TRUE	15	34848715	34848959	0,511	-0,919703128 0
SP52	T41	SP52T40	TRUE	15	35141453	101933258	0,800173014	-0,69074011
SP52	T40	SP52T40	TRUE	15	101968084	102304770	0,571	-1,151068556 0
SP52	T4	SP52T40	TRUE	16	81639	90109711	0,5	-0,032209648 1 1
SP52	T4	SP52T40	TRUE	17	6115	30822034	0,507	-0,014946459 1 1
SP52	T40	SP52T40	FALSE	17	31319033	33977538	0,793	-0,686054964 1
SP52	T41	SP52T40	TRUE	17	33998904	34067892	0,526	-0,073618152 1
SP52	T40	SP52T40	TRUE	17	34097039	35783812	0,797	-0,700131337 1
SP52	T41	SP52T40	TRUE	17	35896123	36398000	0,502	-0,152274116 1

SP52	T41	SP52T40	17	36520567	40375309	0,786314949	-0,787474669	TRUE
SP52	T41	SP52T4TRUE	17	41046440	81006629	0,5	-0,029886797	1
SP52	T41	SP52T4TRUE	18	12893	77893683	0,5	0,028092274	1
SP52	T41	SP52T4TRUE	19	291184	50542359	0,5	-0,088585686	1
SP52	T41	SP52T4TRUE	19	50562372	58991638	0,642	0,417375691	2
SP52	T41	SP52T4FALSE	20	168781	62904542	0,6525	0,421885855	2
SP52	T41	SP52T4TRUE	21	9912042	48083526	0,504	-0,013741353	1
SP52	T41	SP52T4TRUE	22	16348231	51211392	0,502	-0,041046298	1
SP54	M11	SP54M1TRUE	1	139213	249148399	0,5	0,059531461	1
SP54	M11	SP54M1TRUE	2	224919	242842568	0,5	-0,008361634	1
SP54	M11	SP54M1TRUE	3	361508	197804058	0,5	-0,030223695	1
SP54	M11	SP54M1TRUE	4	64892	191033653	0,5	-0,030166905	1
SP54	M11	SP54M1TRUE	5	163205	180687212	0,5	0,053978258	1
SP54	M11	SP54M1TRUE	6	312023	32557339	0,5	0,019218232	1
SP54	M10	SP54M1FALSE	6	32557365	32605451	0,687	-0,09311811	1
SP54	M11	SP54M1TRUE	6	32609009	170190659	0,5	-0,011757484	1
SP54	M11	SP54M1TRUE	7	286402	53854818	0,5	0,041127114	1
SP54	M11	SP54M1FALSE	7	54610293	55242609	0,7115	1,00646511	3
SP54	M11	SP54M1TRUE	7	55433880	159024799	0,5	0,036021946	1
SP54	M11	SP54M1TRUE	8	182934	27729713	0,5	0,024706978	1
SP54	M10	SP54M1FALSE	8	27776285	27776335	0,818	0,351132624	2
SP54	M11	SP54M1TRUE	8	27779811	146229040	0,503	0,00479506	1
SP54	M11	SP54M1TRUE	9	117713	141071475	0,505	-0,010257137	1

SP54	M11	SP54M1 TRUE	10	282897	18691018	0,5	-0,127703592	1
SP54	M10	SP54M1 FALSE	10	18697657	18828663	0,689	-0,467699966	1
SP54	M11	SP54M1 TRUE	10	18837285	135281637	0,5	-0,076033158	1
SP54	M11	SP54M1 TRUE	11	193096	134856661	0,5	-0,004270337	1
SP54	M1TRUE	SP54M1	12	92252	57588838	0,505	-0,020059389	1 1
SP54	M11	SP54M1 TRUE	12	58089413	58217927	0,82	1,540675908	5
SP54	M11	SP54M1 TRUE	12	58335626	114261053	0,5	-0,065923463	1
SP54	M11	SP54M1 TRUE	12	114261237	133758539	0,503	-0,098826186	1
SP54	M11	SP54M1 TRUE	13	19042581	115064542	0,5	-0,037525139	1
SP54	M11	SP54M1 TRUE	14	19188622	107170207	0,5	-0,016817381	1
SP54	M11	SP54M1 TRUE	15	20173160	102304498	0,5	-0,033933809	1
SP54	M1TRUE	SP54M1	16	97610	90161753	0,5	-0,039172637	1 1
SP54	M1FALSE	SP54M1	17	6115	39305956	0,554	-0,004604679	1 1
SP54	M11	SP54M1 FALSE	17	39383012	39394807	0,767	0,506528725	2
SP54	M11	SP54M1 TRUE	17	39406409	81083660	0,5	0,021168054	1
SP54	M11	SP54M1 TRUE	18	196829	77736579	0,5	-0,031151721	1
SP54	M11	SP54M1 TRUE	19	288246	59059729	0,5	-0,000239319	1
SP54	M11	SP54M1 TRUE	20	239688	62904542	0,5	-0,022765765	1
SP54	M11	SP54M1 TRUE	21	9907097	11181645	0,538	-0,068477369	1
SP54	M11	SP54M1 TRUE	21	14418486	48080896	0,5	-0,001420144	1
SP54	M11	SP54M1 TRUE	22	16366264	51183255	0,5	-0,013556929	1
SP54	T11	SP54T1 FALSE	1	139213	249148399	0,574	0,106157138	2
SP54	T11	SP54T1 TRUE	2	224919	242842568	0,5	-0,126049784	1

SP54	T11	SP54T1TRUE	3	361508	47762030	0,5	-0,097517954	1
SP54	T11	SP54T1TRUE	3	47770380	49463287	0,612	0,175691827	2
SP54	T11	SP54T1TRUE	3	49570882	197804058	0,5	-0,127872505	1
SP54	T1TRUE	SP54T1	4	64892	191033653	0,5	-0,158164205	1 1
SP54	T11	SP54T1FALSE	5	163205	180687212	0,653	0,182811874	2
SP54	T11	SP54T1TRUE	6	312023	32546965	0,5	-0,091991408	1
SP54	T11	SP54T1FALSE	6	32547019	32629859	0,596	0,027879633	2
SP54	T11	SP54T1FALSE	6	32634331	32709346	0,7	-0,065767528	2
SP54	T11	SP54T1TRUE	6	32713030	170190659	0,503	-0,105768168	1
SP54	T11	SP54T1TRUE	7	286402	53854818	0,623	0,297344244	2
SP54	T12	SP54T1FALSE	7	54610293	55242609	0,874	2,275369161	14
SP54	T11	SP54T1TRUE	7	55433880	57529392	0,628	0,274518117	2
SP54	T11	SP54T1FALSE	7	62599308	102874211	0,597	0,253994868	2
SP54	T11	SP54T1TRUE	7	102898934	159024799	0,619	0,286702875	2
SP54	T11	SP54T1TRUE	8	182934	146229040	0,5	-0,029080445	1
SP54	T11	SP54T1TRUE	9	117713	141071475	0,5	-0,054795458	1
SP54	T10	SP54T1FALSE	10	282897	51592727	0,764	-0,432452037	1
SP54	T11	SP54T1TRUE	10	51623004	51633027	0,52	-0,391979943	1
SP54	T10	SP54T1FALSE	10	52086939	135281637	0,7655	-0,391073586	1
SP54	T11	SP54T1TRUE	11	193096	134856661	0,5025	-0,113522811	1
SP54	T1TRUE	SP54T1	12	92252	57588838	0,5	-0,097440052	1 1
SP54	T11	SP54T1TRUE	12	58089413	58217927	0,964	3,603725081	40
SP54	T11	SP54T1TRUE	12	58335626	133758539	0,5	-0,106318805	1

SP54	T11	SP54T1	13	19042581	115064542	0,54	-0,404915631	1 FALSE
SP54	T11	SP54T1	14	19188622	107170207	0,504	-0,095986387	1 TRUE
SP54	T11	SP54T1	15	20173160	42632262	0,5	-0,300423152	1 TRUE
SP54	T11	SP54T1	15	42635124	42635160	0,640487744	-1,043518223	0 TRUE
SP54	T11	SP54T1	15	42635395	102304498	0,5	-0,231412396	1 TRUE
SP54	T11	SP54T1	16	97610	32630184	0,5	-0,092649673	1 TRUE
SP54	T10	SP54T1	16	32633233	33424638	0,667	-0,406418128	1 FALSE
SP54	T11	SP54T1	16	33489895	90161753	0,5	-0,06446769	1 TRUE
SP54	T11	SP54T1	17	6115	13928093	0,7015	0,086237585	2 FALSE
SP54	T11	SP54T1	17	13928124	21206556	0,657	0,267307194	2 FALSE
SP54	T11	SP54T1	17	21312562	21319943	0,515	0,151603262	1 TRUE
SP54	T11	SP54T1	17	21407858	81083660	0,658	0,168173889	2 FALSE
SP54	T11	SP54T1	18	196829	77736579	0,5	-0,145610496	1 TRUE
SP54	T11	SP54T1	19	288246	59059729	0,6225	0,305975527	2 TRUE
SP54	T11	SP54T1	20	239688	62904542	0,505	-0,099927062	1 TRUE
SP54	T11	SP54T1	21	9907097	48080896	0,5	-0,21430452	1 TRUE
SP54	T11	SP54T1	22	16366264	51183255	0,5	-0,056482688	1 TRUE
SP54	T21	SP54T2	1	139213	121124362	0,627	0,278108986	2 TRUE
SP54	T22	SP54T2	1	142634897	145115810	0,503	0,402431648	2 TRUE
SP54	T21	SP54T2	1	145298186	249148399	0,629	0,305218018	2 TRUE
SP54	T21	SP54T2	2	224919	240923050	0,504	-0,081574528	1 TRUE
SP54	T20	SP54T2	2	240946766	242842568	0,673	-0,60464776	1 FALSE
SP54	T21	SP54T2	3	361508	47770380	0,5	-0,086648628	1 TRUE

SP54	T21	SP54T21	3	47953405	49570882	0,617	0,21306555	2
SP54	T21	SP54T21	3	49689210	197804058	0,504	-0,089851589	1
SP54	T2TRUE	SP54T2	4	64892	191033653	0,5	-0,085427563	1
SP54	T21	SP54T21	5	163205	180687212	0,628	0,303815269	2
SP54	T21	SP54T21	6	312023	32557655	0,5	-0,079747728	1
SP54	T210	SP54T2TRUE	6	32605189	32605451	0,742699116	-0,6623922	
SP54	T21	SP54T21	6	32609009	32628835	0,6	0,004930615	2
SP54	T21	SP54T21	6	32628841	170190659	0,502	-0,080227796	1
SP54	T21	SP54T21	7	286402	57529392	0,628	0,317207758	2
SP54	T21	SP54T21	7	62599308	91570290	0,5	-0,05648795	1
SP54	T21	SP54T21	7	91599825	147926734	0,63	0,303036435	2
SP54	T21	SP54T21	7	147926888	151478187	0,691	0,549404203	3
SP54	T21	SP54T21	7	151483445	159024799	0,653	0,247827716	2
SP54	T21	SP54T21	8	182934	146229040	0,5	-0,067044937	1
SP54	T21	SP54T21	9	117713	141071475	0,556	0,103886054	1
SP54	T20	SP54T2FALSE	10	282897	51592727	0,792	-0,379113867	1
SP54	T21	SP54T21	10	51623004	51633027	0,518	-0,103795068	1
SP54	T210	SP54T2FALSE	10	52086939	135281637	0,793634998	-0,344134104	
SP54	T21	SP54T21	11	193096	134856661	0,5	-0,087906586	1
SP54	T2TRUE	SP54T2	12	92252	57588838	0,5	-0,078841621	1
SP54	T21	SP54T21	12	58089413	58217927	0,957	3,527804657	35
SP54	T21	SP54T21	12	58335626	133758539	0,5	-0,113295633	1
SP54	T21	SP54T21	13	19042581	115064542	0,5	-0,140300703	1

SP54	T21	SP54T2TRUE	14	19188622	107170207	0,5	-0,094327288	1
SP54	T21	SP54T2TRUE	15	20173160	102304498	0,505	-0,218383951	1
SP54	T2TRUE	SP54T2TRUE	16	97610	57057679	0,505	-0,148525348	1
SP54	T21	SP54T2FALSE	16	57062177	57551966	0,6365	0,352835527	2
SP54	T21	SP54T2TRUE	16	57552088	90161753	0,5	-0,119940456	1
SP54	T20	SP54T2TRUE	17	6115	12018851	0,825039686	-0,1059635	2
SP54	T21	SP54T2FALSE	17	12606826	21312678	0,653	0,260018205	2
SP54	T21	SP54T2TRUE	17	21318586	21519033	0,506	0,297857972	1
SP54	T21	SP54T2FALSE	17	21535937	81083660	0,661	0,280313564	2
SP54	T21	SP54T2TRUE	18	196829	74962645	0,5	-0,082579813	1
SP54	T21	SP54T2TRUE	18	76934104	77736579	0,661	0,342897124	2
SP54	T21	SP54T2TRUE	19	288246	59059729	0,627	0,227565759	2
SP54	T21	SP54T2TRUE	20	239688	62904542	0,5	-0,10979866	1
SP54	T21	SP54T2TRUE	21	9907097	48080896	0,5	-0,123955891	1
SP54	T21	SP54T2TRUE	22	16366264	51183255	0,5	-0,15123928	1
SP54	T31	SP54T3FALSE	1	139213	120611876	0,583	0,134620442	2
SP54	T30	SP54T3TRUE	1	121115761	142634897	0,758	-0,035850793	2
SP54	T31	SP54T3TRUE	1	143767643	145075854	0,507	0,113528612	1
SP54	T31	SP54T3FALSE	1	145075923	249148399	0,588	0,115700244	2
SP54	T31	SP54T3TRUE	2	224919	242842568	0,507	-0,164436167	1
SP54	T31	SP54T3TRUE	3	361508	197804058	0,5	-0,175327125	1
SP54	T3TRUE	SP54T3TRUE	4	64892	191033653	0,5	-0,211756426	1
SP54	T31	SP54T3FALSE	5	163205	180687212	0,584	0,092496674	2

SP54	T31	SP54T3 TRUE	6	312023	29855401	0,5	-0,164367199	1
SP54	T30	SP54T3 TRUE	6	29855856	29855864	0,773	0,019723311	2
SP54	T31	SP54T3 TRUE	6	29855940	32627976	0,5	-0,012423113	1
SP54	T31	SP54T3 FALSE	6	32627992	32629331	0,6535	0,087074786	2
SP54	T31	SP54T3 TRUE	6	32629380	170190659	0,5	-0,16249618	1
SP54	T31	SP54T3 FALSE	7	286402	53854818	0,584	0,136996013	2
SP54	T32	SP54T3 TRUE	7	54610293	55242609	0,8355	2,102363522	12
SP54	T31	SP54T3 TRUE	7	55433880	91503228	0,5	-0,099522633	1
SP54	T31	SP54T3 FALSE	7	91570290	159024799	0,596	0,155254304	2
SP54	T31	SP54T3 TRUE	8	182934	146229040	0,5	-0,147135256	1
SP54	T31	SP54T3 TRUE	9	117713	141071475	0,5	0,008358764	1
SP54	T30	SP54T3 FALSE	10	282897	51623866	0,661	-0,354938466	1
SP54	T31	SP54T3 TRUE	10	51631453	51633027	0,5	-0,17023817	1
SP54	T30	SP54T3 FALSE	10	52086939	135281637	0,672	-0,301955157	1
SP54	T31	SP54T3 TRUE	11	193096	134856661	0,5	-0,115705129	1
SP54	T3 TRUE	SP54T3	12	92252	57588838	0,5	-0,151226574	1 1
SP54	T31	SP54T3 TRUE	12	58089413	58217927	0,935	2,841700292	21
SP54	T31	SP54T3 TRUE	12	58335626	133758539	0,5	-0,180690566	1
SP54	T31	SP54T3 TRUE	13	19042581	115064542	0,5	-0,270494743	1
SP54	T31	SP54T3 TRUE	14	19188622	107170207	0,505	-0,119921344	1
SP54	T31	SP54T3 TRUE	15	20173160	102304498	0,5	-0,166821801	1
SP54	T3 TRUE	SP54T3	16	97610	90161753	0,5	-0,037486075	1 1
SP54	T3 FALSE	SP54T3	17	6115	12620897	0,722	0,063287738	2 0

SP54	T31	SP54T3 FALSE	17	12799985	81083660	0,649	0,227955523	2
SP54	T31	SP54T3 TRUE	18	196829	74962645	0,5	-0,228218013	1
SP54	T31	SP54T3 TRUE	18	76934104	77513841	0,714	0,723231582	3
SP54	T31	SP54T3 TRUE	18	77703299	77736579	0,519	0,143670734	1
SP54	T31	SP54T3 FALSE	19	288246	7572169	0,59	0,306198776	2
SP54	T30	SP54T3 TRUE	19	7573098	7573301	0,769	-0,218557241	1
SP54	T31	SP54T3 FALSE	19	7584483	59059729	0,586	0,224713257	2
SP54	T31	SP54T3 FALSE	20	239688	25900078	0,51	-0,104296783	1
SP54	T31	SP54T3 TRUE	20	29449333	62904542	0,5	-0,038553697	1
SP54	T31	SP54T3 TRUE	21	9907097	15516898	0,531	-0,287996656	1
SP54	T31	SP54T3 TRUE	21	15516948	45978592	0,5	-0,112229135	1
SP54	T30	SP54T3 FALSE	21	46057391	46057634	0,786	-0,135192383	2
SP54	T31	SP54T3 TRUE	21	46058060	48080896	0,5	0,043896449	1
SP54	T31	SP54T3 TRUE	22	16366264	51183255	0,5	-0,020572771	1
SP54	T41	SP54T4 TRUE	1	139213	16910064	0,643	0,379045018	2
SP54	T41	SP54T4 TRUE	1	16918502	17273444	0,507	0,345588973	1
SP54	T41	SP54T4 TRUE	1	17531582	121124362	0,65	0,362434385	2
SP54	T42	SP54T4 TRUE	1	142634897	145507826	0,507	0,419734505	2
SP54	T41	SP54T4 TRUE	1	145517561	249148399	0,65	0,38719288	2
SP54	T41	SP54T4 TRUE	2	224919	90458594	0,5	-0,155855114	1
SP54	T41	SP54T4 FALSE	2	91678867	92129749	0,6135	-0,066167532	2
SP54	T41	SP54T4 TRUE	2	95527944	240923050	0,5	-0,14223026	1
SP54	T41	SP54T4 0 FALSE	2	240946766	242842568	0,8559983	-0,979298047	

SP54	T41	SP54T4 TRUE	3	361508	47770380	0,5	-0,125574874	1
SP54	T41	SP54T4 TRUE	3	47953405	49463287	0,665	0,359603884	2
SP54	T41	SP54T4 TRUE	3	49570882	197804058	0,505	-0,111158396	1
SP54	T41	SP54T4 TRUE	4	64892	49553059	0,5	-0,123055865	1
SP54	T41	SP54T4 TRUE	4	52714244	191033653	0,507	-0,143122043	1
SP54	T41	SP54T4 FALSE	5	163205	180687212	0,639	0,291992424	2
SP54	T41	SP54T4 TRUE	6	312023	29855401	0,5	-0,07832865	1
SP54	T40	SP54T4 FALSE	6	29855856	29855864	0,767	-0,624196151	1
SP54	T41	SP54T4 TRUE	6	29855940	170190659	0,5	-0,107980554	1
SP54	T41	SP54T4 TRUE	7	286402	57529392	0,656	0,401428714	2
SP54	T41	SP54T4 TRUE	7	62599308	90747315	0,507	-0,171483677	1
SP54	T41	SP54T4 TRUE	7	91503228	159024799	0,65	0,360738752	2
SP54	T41	SP54T4 TRUE	8	182934	100994389	0,5	-0,11245366	1
SP54	T41	SP54T4 TRUE	8	100999575	101542205	0,658	0,411304034	2
SP54	T41	SP54T4 TRUE	8	101586133	146229040	0,5	-0,068747259	1
SP54	T41	SP54T4 FALSE	9	117713	141071475	0,571	0,162368315	1
SP54	T410	SP54T4 FALSE	10	282897	30902048	0,887924781	-0,617679522	
SP54	T41	SP54T4 TRUE	10	30915618	30915906	0,625	-0,641135316	1
SP54	T410	SP54T4 FALSE	10	30960716	51592727	0,891303015	-0,57352413	
SP54	T41	SP54T4 TRUE	10	51623004	51633027	0,5	-0,296339162	1
SP54	T410	SP54T4 FALSE	10	52086939	135281637	0,894379096	-0,532107602	
SP54	T41	SP54T4 TRUE	11	193096	134856661	0,503	-0,097990134	1
SP54	T41	SP54T4 TRUE	12	92252	57588838	0,5	-0,108422257	1

SP54	T41	SP54T41 TRUE	12	58089413	58217927	0,959	3,530081045	28
SP54	T41	SP54T41 TRUE	12	58335626	133758539	0,5	-0,133725453	1
SP54	T41	SP54T41 TRUE	13	19042581	115064542	0,5	-0,145924094	1
SP54	T41	SP54T41 TRUE	14	19188622	107170207	0,5	-0,102270664	1
SP54	T41	SP54T41 FALSE	15	20173160	22145401	0,577	-0,803967666	1
SP54	T40	SP54T40 FALSE	15	22345038	42619508	0,7	-0,591444568	1
SP54	T41	SP54T41 TRUE	15	42630896	42696158	0,5	-0,725830815	1
SP54	T40	SP54T40 FALSE	15	42698291	50087964	0,71	-0,59275281	1
SP54	T41000	SP54T41000 TRUE	15	50152166	50152274	0,999813597	-1,150695739	
SP54	T40	SP54T40 FALSE	15	50158695	102304498	0,692	-0,61332404	1
SP54	T4FALSE	SP54T4FALSE	16	97610	56928470	0,559	-0,322798516	1
SP54	T41	SP54T41 FALSE	16	56994528	57159402	0,736	0,244806746	2
SP54	T41	SP54T41 FALSE	16	57494178	72991286	0,541	-0,250171472	1
SP54	T41	SP54T41 FALSE	16	72993831	74666634	0,71	0,272257762	2
SP54	T41	SP54T41 FALSE	16	74694692	90161753	0,574	-0,310128446	1
SP54	T40	SP54T40 TRUE	17	6115	12018851	0,920936654	-0,114293119	2
SP54	T41	SP54T41 TRUE	17	12606826	21206556	0,659	0,433987565	2
SP54	T42	SP54T42 TRUE	17	21312562	21319943	0,505	0,514897882	2
SP54	T41	SP54T41 FALSE	17	21407858	81083660	0,667	0,431178451	2
SP54	T41	SP54T41 TRUE	18	196829	77736579	0,5	-0,107060216	1
SP54	T41	SP54T41 TRUE	19	288246	59059729	0,653	0,383416011	2
SP54	T41	SP54T41 TRUE	20	239688	62904542	0,5	-0,105229471	1
SP54	T41	SP54T41 FALSE	21	9907097	11181645	0,572	-0,30980393	1

SP54	T41	SP54T4 TRUE	21	14418486	48080896	0,5	-0,138873604	1
SP54	T41	SP54T4 TRUE	22	16366264	51183255	0,5	-0,112902959	1
SP54	T51	SP54T5 TRUE	1	139213	16902894	0,653	0,290409084	2
SP54	T51	SP54T5 TRUE	1	16910064	17531582	0,505	0,387212594	1
SP54	T51	SP54T5 FALSE	1	17550303	121124362	0,667	0,345258582	2
SP54	T51	SP54T5 TRUE	1	142634897	145109583	0,505	0,428054845	1
SP54	T51	SP54T5 FALSE	1	145109897	249148399	0,664	0,343388528	2
SP54	T51	SP54T5 TRUE	2	224919	240923050	0,5	-0,140545538	1
SP54	T50	SP54T5 TRUE	2	240946766	242842568	0,889	-0,957780695	1
SP54	T51	SP54T5 TRUE	3	361508	47770380	0,5	-0,076518152	1
SP54	T51	SP54T5 FALSE	3	47953405	48463711	0,667	0,465235189	2
SP54	T51	SP54T5 TRUE	3	48474249	197804058	0,5	-0,062588998	1
SP54	T5TRUE	SP54T5	4	64892	191033653	0,502	-0,077866015	1 1
SP54	T51	SP54T5 FALSE	5	163205	180687212	0,626	0,266757589	2
SP54	T51	SP54T5 TRUE	6	312023	32557655	0,5	-0,070059332	1
SP54	T50	SP54T5 TRUE	6	32605189	32605451	0,85	-0,269879531	1
SP54	T51	SP54T5 FALSE	6	32609009	32724305	0,575	-0,015166353	1
SP54	T51	SP54T5 TRUE	6	32724312	170190659	0,5	-0,066692776	1
SP54	T51	SP54T5 TRUE	7	286402	54610293	0,645	0,422124052	2
SP54	T51	SP54T5 TRUE	7	54614582	55242609	0,782	1,093409534	4
SP54	T51	SP54T5 TRUE	7	55433880	57529392	0,647	0,412669111	2
SP54	T51	SP54T5 TRUE	7	62599308	90747315	0,5	-0,090976248	1
SP54	T51	SP54T5 FALSE	7	91503228	159024799	0,635	0,387521916	2

SP54	T51	SP54T51 TRUE	8	182934	27729713	0,5	-0,070375966	1
SP54	T50	SP54T50 FALSE	8	27776285	27776335	0,8055	-0,970533304	0
SP54	T51	SP54T51 TRUE	8	27779811	100994389	0,505	-0,075939224	1
SP54	T51	SP54T51 TRUE	8	100999575	101542205	0,679	0,462957479	2
SP54	T51	SP54T51 FALSE	8	101586133	146229040	0,513	-0,049178896	1
SP54	T51	SP54T51 TRUE	9	117713	141071475	0,506	0,068608921	1
SP54	T51	SP54T51 0 TRUE	10	282897	51592727	0,900178979	-0,724490406	
SP54	T51	SP54T51 TRUE	10	51623004	51633027	0,512	-0,467290572	1
SP54	T51	SP54T51 0 TRUE	10	52086939	135281637	0,902677697	-0,687917213	
SP54	T51	SP54T51 TRUE	11	193096	134856661	0,5	-0,093395159	1
SP54	T5 TRUE	SP54T5	12	92252	57588838	0,5	-0,063689382	1 1
SP54	T51	SP54T51 TRUE	12	58089413	58217927	0,948	3,280494297	22
SP54	T51	SP54T51 TRUE	12	58335626	133758539	0,5	-0,079174779	1
SP54	T51	SP54T51 TRUE	13	19042581	115064542	0,5	-0,0973199	1
SP54	T51	SP54T51 TRUE	14	19188622	107170207	0,5	-0,057897593	1
SP54	T50	SP54T50 TRUE	15	20173160	20477289	0,517	-1,154681573	0
SP54	T51	SP54T51 0 TRUE	15	21137321	21902874	0,863910309	-1,171632628	
SP54	T51	SP54T51 TRUE	15	21903156	21938082	0,515	-0,926285504	1
SP54	T50	SP54T50 FALSE	15	21938163	34813947	0,869	-0,904503279	1
SP54	T51	SP54T51 TRUE	15	34848553	34848887	0,538	-0,777141349	1
SP54	T50	SP54T50 FALSE	15	35044757	77907784	0,873	-0,862287314	1
SP54	T51	SP54T51 TRUE	15	78189163	78191543	0,571	-0,895654548	1
SP54	T50	SP54T50 FALSE	15	78208880	102304498	0,869	-0,870113888	1

SP54	T5	SP54T5	16	97610	56928470	0,594	-0,348619447	1	1
	FALSE								
SP54	T5	SP54T5	16	56994528	57503773	0,7545	0,249794262	2	
	1	FALSE							
SP54	T5	SP54T5	16	57551966	72993831	0,597	-0,31334436	1	
	1	FALSE							
SP54	T5	SP54T5	16	74321225	74695079	0,725	0,283119995	2	
	1	FALSE							
SP54	T5	SP54T5	16	74706298	90161753	0,595	-0,349828771	1	
	1	FALSE							
SP54	T5	SP54T5	17	6115	12018851	0,935442625	-0,095728673	2	
	0	TRUE							
SP54	T5	SP54T5	17	12606826	21206556	0,661	0,44301319	2	
	1	TRUE							
SP54	T5	SP54T5	17	21312562	21319943	0,515	0,425145257	1	
	1	TRUE							
SP54	T5	SP54T5	17	21407858	81083660	0,665	0,457872385	2	
	1	FALSE							
SP54	T5	SP54T5	18	196829	77736579	0,5	-0,041777376	1	
	1	TRUE							
SP54	T5	SP54T5	19	288246	59059729	0,654	0,43101189	2	
	1	TRUE							
SP54	T5	SP54T5	20	239688	62904542	0,5	-0,068361072	1	
	1	TRUE							
SP54	T5	SP54T5	21	9907097	14917610	0,522	-0,170018399	1	
	1	TRUE							
SP54	T5	SP54T5	21	15281853	15281957	0,775	-0,456332739	1	
	0	FALSE							
SP54	T5	SP54T5	21	15289026	48080896	0,5	-0,069011434	1	
	1	TRUE							
SP54	T5	SP54T5	22	16366264	51183255	0,5	-0,089410712	1	
	1	TRUE							
SP54	T6	SP54T6	1	139213	121124362	0,573	0,350694207	2	
	1	FALSE							
SP54	T6	SP54T6	1	142634897	146791020	0,511	0,358719616	2	
	2	TRUE							
SP54	T6	SP54T6	1	146791289	249148399	0,58	0,347716569	2	
	1	FALSE							
SP54	T6	SP54T6	2	224919	240923050	0,503	-0,077173984	1	
	1	TRUE							
SP54	T6	SP54T6	2	240946766	242842568	0,621	-0,450958826	1	
	0	FALSE							
SP54	T6	SP54T6	3	361508	47770380	0,5	-0,102382164	1	
	1	TRUE							
SP54	T6	SP54T6	3	47953405	48474249	0,65	0,430596744	2	
	1	TRUE							

SP54	T61	SP54T6 TRUE	3	48481647	197804058	0,5	-0,079605277	1
SP54	T6 TRUE	SP54T6	4	64892	1388413	0,51	-0,124097946	1
SP54	T60	SP54T6 TRUE	4	1389070	1389156	0,75	-0,388387611	1
SP54	T61	SP54T6 TRUE	4	1397611	191033653	0,5	-0,122449595	1
SP54	T61	SP54T6 TRUE	5	163205	180687212	0,625	0,314480958	2
SP54	T61	SP54T6 TRUE	6	312023	32489792	0,5	-0,086729748	1
SP54	T60	SP54T6 FALSE	6	32489825	32489973	0,761	0,313060142	2
SP54	T61	SP54T6 FALSE	6	32497905	32634508	0,59	-0,000880691	2
SP54	T61	SP54T6 TRUE	6	32634514	170190659	0,504	-0,088412206	1
SP54	T61	SP54T6 FALSE	7	286402	53854818	0,665	0,284690532	2
SP54	T61	SP54T6 TRUE	7	54610293	55242609	0,8105	1,366855773	6
SP54	T61	SP54T6 FALSE	7	55433880	57529392	0,662	0,243087085	2
SP54	T61	SP54T6 FALSE	7	62599308	91671853	0,589	0,037687994	2
SP54	T61	SP54T6 FALSE	7	91674302	147674912	0,667	0,307453543	2
SP54	T61	SP54T6 TRUE	7	147926734	151478187	0,855	1,385720086	7
SP54	T61	SP54T6 FALSE	7	151483445	159024799	0,667	0,231105341	2
SP54	T61	SP54T6 TRUE	8	182934	146229040	0,5	-0,091509896	1
SP54	T61	SP54T6 TRUE	9	117713	141071475	0,5	-0,037906383	1
SP54	T60	SP54T6 TRUE	10	282897	49763618	0,789	-0,66701184	1
SP54	T60	SP54T6 TRUE	10	49763677	49763717	0,5	-0,841891441	0
SP54	T60	SP54T6 TRUE	10	49790972	51623004	0,786	-0,608482227	1
SP54	T61	SP54T6 TRUE	10	51623061	51633027	0,556	-0,422287227	1
SP54	T60	SP54T6 FALSE	10	52086939	135281637	0,794	-0,655945531	1

SP54	T61	SP54T61 TRUE	11	193096	82443817	0,5	-0,086851617	1
SP54	T60	SP54T60 TRUE	11	82444021	82444226	0,553	-1,517927173	0
SP54	T61	SP54T61 TRUE	11	82704967	134856661	0,5	-0,070703674	1
SP54	T6TRUE	SP54T6TRUE	12	92252	57588838	0,5	-0,076761684	1 1
SP54	T61	SP54T61 TRUE	12	58089413	58217927	0,97	4,024232585	46
SP54	T61	SP54T61 TRUE	12	58335626	133758539	0,5	-0,080000247	1
SP54	T61	SP54T61 TRUE	13	19042581	115064542	0,507	-0,321914125	1
SP54	T61	SP54T61 TRUE	14	19188622	107170207	0,5	-0,129953269	1
SP54	T61	SP54T61 TRUE	15	20173160	102304498	0,5	-0,199763179	1
SP54	T6TRUE	SP54T6TRUE	16	97610	31580272	0,5045	-0,099901472	1 1
SP54	T61	SP54T61 FALSE	16	31580530	33424637	0,608	-0,428444744	1
SP54	T61	SP54T61 TRUE	16	33424638	56928470	0,506	-0,190489076	1
SP54	T61	SP54T61 TRUE	16	56994528	57499902	0,629	0,284546025	2
SP54	T61	SP54T61 TRUE	16	57503213	72993831	0,5	-0,023386436	1
SP54	T61	SP54T61 TRUE	16	74321225	74695079	0,656	0,448763976	2
SP54	T61	SP54T61 TRUE	16	74706298	90161753	0,5	-0,112997932	1
SP54	T60	SP54T60 FALSE	17	6115	12018851	0,879284866	0,150144284	2
SP54	T60	SP54T60 FALSE	17	12606826	21206556	0,734	0,335110719	2
SP54	T61	SP54T61 TRUE	17	21312562	21319943	0,52	0,302582366	1
SP54	T61	SP54T61 FALSE	17	21407858	44160050	0,741	0,390231384	3
SP54	T62	SP54T62 TRUE	17	44344822	44626347	0,54	0,942820566	2
SP54	T61	SP54T61 FALSE	17	44788310	81083660	0,742	0,386177481	3
SP54	T61	SP54T61 TRUE	18	196829	77736579	0,505	-0,080843653	1

SP54	T61	SP54T61	19	288246	24115369	0,624	0,379367342	2	TRUE
SP54	T61	SP54T61	19	28418794	59059729	0,632	0,352618497	2	TRUE
SP54	T61	SP54T61	20	239688	62904542	0,5	-0,077177387	1	TRUE
SP54	T61	SP54T61	21	9907097	14917610	0,514	-0,129738324	1	TRUE
SP54	T60	SP54T60	21	15281853	15481365	0,701	-0,377202386	1	FALSE
SP54	T61	SP54T61	21	15516330	48080896	0,5	-0,090089871	1	TRUE
SP54	T61	SP54T61	22	16366264	48023297	0,5	-0,100466352	1	TRUE
SP54	T60	SP54T60	22	48896580	48972536	0,676	-0,798832821	1	TRUE
SP54	T61	SP54T61	22	49176220	51183255	0,52	-0,209896557	1	TRUE
SP55	S	SP55S 1	69511	249141454	0,5	-0,024949102	1	1	TRUE
SP55	S	SP55S 2	41366	242842568	0,504	-0,025000225	1	1	TRUE
SP55	S	SP55S 3	361493	193220219	0,503	-0,00145555	1	1	TRUE
SP55	S	SP55S 3	194080648	194387300	0,6475	0,414464978	2	1	FALSE
SP55	S	SP55S 3	194390617	197838039	0,5	-0,022629652	1	1	TRUE
SP55	S	SP55S 4	60400	190863027	0,5	-0,01905845	1	1	TRUE
SP55	S	SP55S 5	181660	180582604	0,5	0,051241995	1	1	TRUE
SP55	S	SP55S 6	203878	32547053	0,503	-0,053987911	1	1	TRUE
SP55	S	SP55S 6	32547980	32548489	0,745	0,30301569	2	0	FALSE
SP55	S	SP55S 6	32548507	32632638	0,582	0,04283656	2	1	FALSE
SP55	S	SP55S 6	32632647	32634192	0,745	-0,293558153	1	0	TRUE
SP55	S	SP55S 6	32634226	170892848	0,5	-0,039749032	1	1	TRUE
SP55	S	SP55S 7	286534	54724286	0,618	0,360443963	2	1	TRUE
SP55	S	SP55S 7	55001472	55272826	0,981	4,673148078	82	1	TRUE
SP55	S	SP55S 7	55466002	57529392	0,63	0,272332662	2	1	FALSE

SP55	S	TRUE	SP55S	7	62669789	158827414	0,622	0,360624437	2	1
SP55	S	TRUE	SP55S	8	183002	146105917	0,5	0,006017259	1	1
SP55	S	TRUE	SP55S	9	214706	3324206	0,51	-0,061316448	1	1
SP55	S	TRUE	SP55S	9	3829188	7174430	0,7345	-0,487829504	1	0
SP55	S	TRUE	SP55S	9	8319806	13987678	0,528	-0,016990308	1	1
SP55	S	0	SP55S	9	14125908	21186931	0,709235192	-0,612694745	1	FALSE
SP55	S	FALSE	SP55S	9	21187121	30559335	0,571	-0,89812396	0	0
SP55	S	0	SP55S	9	31254567	32542204	0,721344808	-0,551323112	1	TRUE
SP55	S	TRUE	SP55S	9	32567655	38453992	0,5	-0,008734777	1	1
SP55	S	FALSE	SP55S	9	40503085	68433462	0,67	-0,296167347	1	0
SP55	S	TRUE	SP55S	9	69002200	141015351	0,5	0,010917562	1	1
SP55	S	TRUE	SP55S	10	93816	5246584	0,728182245	-0,515481769	1	0
SP55	S	TRUE	SP55S	10	5247631	46148326	0,727	-0,542834381	1	0
SP55	S	TRUE	SP55S	10	46272679	47000239	0,509	-0,543979223	1	1
SP55	S	0	SP55S	10	47605468	135279810	0,71996845	-0,558431453	1	TRUE
SP55	S	TRUE	SP55S	11	193096	134244322	0,503	-0,027773883	1	1
SP55	S	TRUE	SP55S	11	134251777	134927578	0,559	-0,657531099	0	0
SP55	S		SP55S	12	92252	133770096	0,5	-0,012591941	1	1 TRUE
SP55	S	TRUE	SP55S	13	19042705	115064542	0,5	-0,073001675	1	1
SP55	S	TRUE	SP55S	14	19118067	107283160	0,505	-0,016426452	1	1
SP55	S	TRUE	SP55S	15	20433755	33446947	0,504	-0,079708518	1	1
SP55	S	FALSE	SP55S	15	33842260	50782703	0,603	-0,281992522	1	0
SP55	S	TRUE	SP55S	15	50821945	102388991	0,5	-0,023273518	1	1

SP55	S	SP55S	16	215106	90161231	0,5	-0,029925088	1	1	TRUE
SP55	S	SP55S	17	6115	81052423	0,5	0,001689916	1	1	TRUE
SP55	S	SP55S	18	166819	77927028	0,5	0,017548664	1	1	TRUE
SP55	S	SP55S	19	311988	43922300	0,619	0,287049754	2	1	TRUE
SP55	S	SP55S	19	43999634	44515514	0,697	0,730307572	3	1	TRUE
SP55	S	SP55S	19	44535999	58806083	0,617	0,290505521	2	1	TRUE
SP55	S	SP55S	20	76962	62903729	0,5	-0,017648174	1	1	TRUE
SP55	S	SP55S	21	9907222	48080896	0,5	-0,042727935	1	1	TRUE
SP55	S	SP55S	22	16287789	51137094	0,5	-0,042127591	1	1	TRUE
SP55	T1	SP55T1	1	69511	225699681	0,5	-0,002011714	1	1	TRUE
SP55	T1	SP55T1	1	225965832	226626684	0,653	-0,3923913	1	0	TRUE
SP55	T1	SP55T1	1	226923706	249141454	0,507	-0,014425251	1	1	TRUE
SP55	T1	SP55T1	2	41366	242842568	0,5	-0,032643545	1	1	TRUE
SP55	T1	SP55T1	3	361493	197838039	0,5	-0,044749782	1	1	TRUE
SP55	T1	SP55T1	4	60400	3526786	0,63	-0,434387649	1	0	FALSE
SP55	T1	SP55T1	4	3589893	190863027	0,504	-0,014109703	1	1	TRUE
SP55	T1	SP55T1	5	181660	180582604	0,504	0,022992562	1	1	TRUE
SP55	T1	SP55T1	6	203878	32546986	0,505	-0,060716053	1	1	TRUE
SP55	T1	SP55T1	6	32547053	32548155	0,724	0,40553771	3	1	TRUE
SP55	T1	SP55T1	6	32548178	32632689	0,571	0,013069808	2	1	FALSE
SP55	T1	SP55T1	6	32632694	32634192	0,719	-0,189263855	1	0	FALSE
SP55	T1	SP55T1	6	32634226	170892848	0,5	-0,047404026	1	1	TRUE
SP55	T1	SP55T1	7	286534	54724286	0,612	0,323564304	2	1	TRUE
SP55	T1	SP55T1	7	55001472	55272826	0,981	4,333687754	73	1	TRUE

SP55	T1	SP55T1	7	55466002	57529392	0,616	0,291917506	2
	1	TRUE						
SP55	T1	SP55T1	7	62669789	158827414	0,609	0,315153022	2
	1	TRUE						
SP55	T1	SP55T1	8	183002	146105917	0,5	-0,025294175	1
	1	TRUE						
SP55	T1	SP55T1	9	214706	3324206	0,522	0,119192333	1
	1	TRUE						
SP55	T1	SP55T1	9	3829188	7105651	0,738542977	-0,23826116	
	1	0	FALSE					
SP55	T1	SP55T1	9	7170006	8521244	0,523	0,099989648	1
	1	TRUE						
SP55	T1	SP55T1	9	12287727	21166004	0,743	-0,15593485	2
	0	FALSE						
SP55	T1	SP55T1	9	21186931	31254567	0,5	-0,537162508	0
	0	TRUE						
SP55	T1	SP55T1	9	31254672	32542204	0,744	-0,177059159	2
	0	TRUE						
SP55	T1	SP55T1	9	32567655	141015351	0,572	0,161130314	2
	1	FALSE						
SP55	T1	SP55T1	10	93816	18691018	0,6895	-0,456363046	1
0	TRUE							
SP55	T1	SP55T1	10	18789724	26518418	0,512	-1,029306716	0
	0	TRUE						
SP55	T1	SP55T1	10	26939401	46952667	0,667	-0,419923532	1
	0	FALSE						
SP55	T1	SP55T1	10	46960084	47000239	0,533	-0,310185235	1
	1	TRUE						
SP55	T1	SP55T1	10	47605468	135279810	0,677	-0,492729699	1
	0	FALSE						
SP55	T1	SP55T1	11	193096	830487	0,512	-0,114962799	1
	1	TRUE						
SP55	T1	SP55T1	11	831122	134927578	0,5	-0,052094842	1
	1	TRUE						
SP55	T1	SP55T1	12	92252	133770096	0,5	-0,015298601	1
1	TRUE							
SP55	T1	SP55T1	13	19042705	115064542	0,503	-0,044818307	1
	1	TRUE						
SP55	T1	SP55T1	14	19118067	107283160	0,505	-0,053377496	1
	1	TRUE						
SP55	T1	SP55T1	15	20433755	102388991	0,5	-0,054537453	1
	1	TRUE						
SP55	T1	SP55T1	16	215106	84907670	0,5	-0,079010267	1
	1	TRUE						
SP55	T1	SP55T1	16	84911195	85722560	0,692808373	-0,470826234	
	1	0	TRUE					

SP55	T1	SP55T1	16	85968282	90161231	0,5	-0,078212677	1
	1	TRUE						
SP55	T1	SP55T1	17	6115	17326605	0,5	-0,019315973	1
	TRUE							
SP55	T1	SP55T1	17	18041507	18243873	0,618	0,324168986	2
	1	TRUE						
SP55	T1	SP55T1	17	18252010	22214959	0,53	-0,053483757	1
	1	FALSE						
SP55	T1	SP55T1	17	25628820	81052423	0,5	-0,043350805	1
	1	TRUE						
SP55	T1	SP55T1	18	166819	77927028	0,5	0,005809685	1
	1	TRUE						
SP55	T1	SP55T1	19	311988	58806083	0,617	0,245842088	2
	1	TRUE						
SP55	T1	SP55T1	20	76962	62903729	0,5	-0,066426179	1
	TRUE							
SP55	T1	SP55T1	21	9907222	48080896	0,5	-0,04781931	1
	1	TRUE						
SP55	T1	SP55T1	22	16287789	43088549	0,5	-0,137521429	1
	1	TRUE						
SP55	T1	SP55T1	22	43088971	51137094	0,66	-0,45927	1
	0	FALSE						
SP55	T2	SP55T2	1	69511	249141454	0,5	-0,056038671	1
	TRUE							
SP55	T2	SP55T2	2	41366	242842568	0,5	-0,047306912	1
	TRUE							
SP55	T2	SP55T2	3	361493	194080916	0,506	-0,035738495	1
	1	TRUE						
SP55	T2	SP55T2	3	194080983	194393034	0,667	0,528419257	2
	1	TRUE						
SP55	T2	SP55T2	3	194999996	197838039	0,511	-0,102232461	1
	1	TRUE						
SP55	T2	SP55T2	4	60400	190863027	0,5	-0,034143456	1
	TRUE							
SP55	T2	SP55T2	5	181660	180582604	0,503	-0,030095268	1
	1	TRUE						
SP55	T2	SP55T2	6	203878	32547053	0,504	-0,083446053	1
	1	TRUE						
SP55	T2	SP55T2	6	32547980	32628845	0,596	0,023473245	2
	1	FALSE						
SP55	T2	SP55T2	6	32628917	170892848	0,5	-0,037748249	1
	1	TRUE						
SP55	T2	SP55T2	7	286534	54724286	0,656	0,484005286	2
	1	TRUE						
SP55	T2	SP55T2	7	55001472	55272826	0,984	4,794898012	66
	1	TRUE						

SP55	T21	SP55T2 TRUE	7	55466002	158827414	0,651	0,482194126	2
SP55	T21	SP55T2 TRUE	8	183002	146105917	0,5	-0,044614127	1
SP55	T21	SP55T2 FALSE	9	214706	3324206	0,596	0,237200594	2
SP55	T22	SP55T20 FALSE	9	3829188	7174430	0,917508588	-0,311778641	
SP55	T21	SP55T2 TRUE	9	8319806	13987678	0,544	0,211132163	1
SP55	T20	SP55T2 FALSE	9	14125908	21166004	0,922	-0,301487496	2
SP55	T20	SP55T2 TRUE	9	21186931	23705108	0,5	-3,167624657	0
SP55	T22	SP55T20 TRUE	9	25677933	26998090	0,921801018	-0,234684539	
SP55	T21	SP55T2 FALSE	9	27195595	30559335	0,623	0,356098346	2
SP55	T20	SP55T2 FALSE	9	31254567	32542204	0,9125	-0,294347912	1
SP55	T21	SP55T2 FALSE	9	32567655	141015351	0,608	0,28172265	2
SP55	T20	SP55T2 TRUE	10	93816	30901628	0,881371568	-0,835912636	1
SP55	T20	SP55T2 FALSE	10	30915882	30978282	0,7	-1,018332016	0
SP55	T20	SP55T2 TRUE	10	30978377	46952667	0,887	-0,833263172	1
SP55	T21	SP55T2 TRUE	10	46960084	47000239	0,526	-0,773328363	1
SP55	T21	SP55T20 TRUE	10	47605468	135279810	0,876847131	-0,88991305	
SP55	T21	SP55T2 TRUE	11	193096	134927578	0,503	-0,058294758	1
SP55	T2 TRUE	SP55T2	12	92252	3948718	0,508	-0,127613801	1 1
SP55	T21	SP55T2 TRUE	12	4388084	4873163	0,638	0,419440616	2
SP55	T21	SP55T2 TRUE	12	4877689	133770096	0,5	-0,040456863	1
SP55	T21	SP55T2 TRUE	13	19042705	115064542	0,504	-0,045709709	1
SP55	T21	SP55T2 TRUE	14	19118067	107283160	0,506	-0,047314194	1
SP55	T21	SP55T2 TRUE	15	20433755	102388991	0,5	-0,074205248	1

SP55	T2	SP55T2	16	215106	90161231	0,5	-0,076114594	1
	1	TRUE						
SP55	T2	SP55T2	17	6115	6607389	0,5	-0,077625156	1
	TRUE							
SP55	T2	SP55T2	17	6610536	7246940	0,665	0,424222215	2
	1	TRUE						
SP55	T2	SP55T2	17	7251605	17326605	0,5	-0,044585321	1
	1	TRUE						
SP55	T2	SP55T2	17	18041507	18291559	0,666	0,436617216	2
	1	TRUE						
SP55	T2	SP55T2	17	18301096	73127217	0,5	-0,033819201	1
	1	TRUE						
SP55	T2	SP55T2	17	73497697	73750847	0,797	1,246933191	4
	1	FALSE						
SP55	T2	SP55T2	17	73811138	81052423	0,5	-0,087330955	1
	1	TRUE						
SP55	T2	SP55T2	18	166819	77927028	0,5	-0,029644232	1
	1	TRUE						
SP55	T2	SP55T2	19	311988	43920612	0,652	0,452750751	2
	1	TRUE						
SP55	T2	SP55T2	19	43922061	44515514	0,73	0,849604191	3
	1	TRUE						
SP55	T2	SP55T2	19	44535999	58806083	0,6565	0,438146096	2
	1	TRUE						
SP55	T2	SP55T2	20	76962	62903729	0,5	-0,059913503	1
	TRUE							
SP55	T2	SP55T2	21	9907222	48080896	0,5	-0,074823262	1
	1	TRUE						
SP55	T2	SP55T2	22	16287789	21424414	0,5	-0,098156396	1
	1	TRUE						
SP55	T2	SP55T2	22	21576082	21983260	0,802	0,292749439	2
	0	TRUE						
SP55	T2	SP55T2	22	22025462	51137094	0,5	-0,059963308	1
	1	TRUE						
SP55	T3	SP55T3	1	69511	26385003	0,508	-0,129319189	1
	TRUE							
SP55	T3	SP55T3	1	26385150	249141454	0,5	-0,038501798	1
	1	TRUE						
SP55	T3	SP55T3	2	41366	242842568	0,5	-0,050369465	1
	TRUE							
SP55	T3	SP55T3	3	361493	197838039	0,5	-0,03436346	1
	1	TRUE						
SP55	T3	SP55T3	4	60400	3231661	0,5975	-0,301669855	1
	TRUE							
SP55	T3	SP55T3	4	3234828	4128926	0,553749626	-0,487048363	
	0	0	FALSE					

SP55	T3	SP55T3	4	4199760	190863027	0,508	-0,03024204	1
	1	TRUE						
SP55	T3	SP55T3	5	181660	180582604	0,503	-0,040015167	1
	1	TRUE						
SP55	T3	SP55T3	6	203878	32489794	0,504	-0,013194752	1
	1	TRUE						
SP55	T3	SP55T3	6	32520683	32628917	0,611	-0,013486201	2
	1	FALSE						
SP55	T3	SP55T3	6	32629193	32632694	0,524	0,084554125	1
	1	TRUE						
SP55	T3	SP55T3	6	32632864	32634192	0,596470412	-0,341869447	
	1	0	TRUE					
SP55	T3	SP55T3	6	32634226	170892848	0,5	-0,025568809	1
	1	TRUE						
SP55	T3	SP55T3	7	286534	54724286	0,574	0,197378501	2
	1	TRUE						
SP55	T3	SP55T3	7	55001472	55272826	0,971	3,752252522	75
	0	TRUE						
SP55	T3	SP55T3	7	55466002	158827414	0,5755	0,195555101	2
	1	TRUE						
SP55	T3	SP55T3	8	183002	146105917	0,5	-0,034842272	1
	1	TRUE						
SP55	T3	SP55T3	9	214706	3324206	0,566	-0,1031661	1
	0	FALSE						
SP55	T3	SP55T3	9	3829188	21029330	0,6245	-0,219013787	1
	0	FALSE						
SP55	T3	SP55T3	9	21166004	141015351	0,5	-0,002180744	1
	1	TRUE						
SP55	T3	SP55T3	10	93816	135279810	0,59869156	-0,333906485	1
	0	TRUE						
SP55	T3	SP55T3	11	193096	134927578	0,5	-0,059467196	1
	1	TRUE						
SP55	T3	SP55T3	12	92252	133770096	0,504	-0,046301115	1
	TRUE							
SP55	T3	SP55T3	13	19042705	115064542	0,5025	-0,044848251	1
	1	TRUE						
SP55	T3	SP55T3	14	19118067	107283160	0,5	-0,046511387	1
	1	TRUE						
SP55	T3	SP55T3	15	20433755	102388991	0,5	-0,056035556	1
	1	TRUE						
SP55	T3	SP55T3	16	215106	90161231	0,5	-0,054615497	1
	1	TRUE						
SP55	T3	SP55T3	17	6115	39389354	0,5	-0,019594752	1
	TRUE							
SP55	T3	SP55T3	17	39394674	39394807	0,5	-0,699126249	0
	0	TRUE						

SP55	T3	SP55T3	17	39406104	81052423	0,5	-0,039800094	1
	1	TRUE						
SP55	T3	SP55T3	18	166819	77927028	0,5	-0,030960523	1
	1	TRUE						
SP55	T3	SP55T3	19	311988	58806083	0,568	0,174956482	2
	1	TRUE						
SP55	T3	SP55T3	20	76962	62903729	0,5	-0,066170341	1
1	TRUE							
SP55	T3	SP55T3	21	9907222	48080896	0,5	-0,055356196	1
	1	TRUE						
SP55	T3	SP55T3	22	16287789	42539105	0,5	-0,117850098	1
	1	TRUE						
SP55	T3	SP55T3	22	42547135	51137094	0,6	-0,307012203	1
	0	TRUE						
SP55	T4	SP55T4	1	69511	12082926	0,589	-0,207137679	1
1	FALSE							
SP55	T4	SP55T4	1	12164391	12253965	0,702793883	-0,867538476	
	1	0	TRUE					
SP55	T4	SP55T4	1	12339744	93306317	0,5	-0,046458968	1
	1	TRUE						
SP55	T4	SP55T4	1	93646418	106435371	0,607	-0,27025167	1
	0	FALSE						
SP55	T4	SP55T4	1	108116051	249141454	0,5	-0,035316968	1
	1	TRUE						
SP55	T4	SP55T4	2	41366	242842568	0,562	0,13151131	1
1	FALSE							
SP55	T4	SP55T4	3	361493	49832788	0,5	-0,030844995	1
	1	TRUE						
SP55	T4	SP55T4	3	49833029	53892641	0,594	-0,272985961	1
	1	FALSE						
SP55	T4	SP55T4	3	53905308	193220219	0,5	-0,02155534	1
	1	TRUE						
SP55	T4	SP55T4	3	194080648	194393034	0,6575	0,431360201	2
	1	FALSE						
SP55	T4	SP55T4	3	194999996	197838039	0,504	-0,122488175	1
	1	TRUE						
SP55	T4	SP55T4	4	60400	190863027	0,5	-0,049117016	1
1	TRUE							
SP55	T4	SP55T4	5	181660	180582604	0,5	-0,046641312	1
	1	TRUE						
SP55	T4	SP55T4	6	203878	32608991	0,506	-0,064252449	1
	1	TRUE						
SP55	T4	SP55T4	6	32609057	32628045	0,676	0,419190171	3
	1	FALSE						
SP55	T4	SP55T4	6	32628420	32632694	0,519	0,212080772	1
	1	TRUE						

SP55	T41	SP55T4	6	32632864	32634263	0,7	0,0441203	2
		FALSE						
SP55	T41	SP55T4	6	32634264	170892848	0,5	-0,048977384	1
		TRUE						
SP55	T41	SP55T4	7	286534	54724286	0,628	0,360546563	2
		TRUE						
SP55	T41	SP55T4	7	55001472	55272826	0,984	4,91007051	91
		TRUE						
SP55	T41	SP55T4	7	55466002	158827414	0,629	0,362965345	2
		TRUE						
SP55	T41	SP55T4	8	183002	146105917	0,5	-0,061040088	1
		TRUE						
SP55	T41	SP55T4	9	214706	3829212	0,52	0,091146666	1
		TRUE						
SP55	T41	SP55T4	9	3932283	7174430	0,785145838	-0,399432391	
		0	FALSE					
SP55	T41	SP55T4	9	8319806	8521244	0,531	0,076175311	1
		TRUE						
SP55	T41	SP55T4	9	12287727	21166004	0,785579109	-0,396520142	
		0	FALSE					
SP55	T40	SP55T4	9	21186931	30559335	0,6	-1,074021929	0
		FALSE						
SP55	T41	SP55T4	9	31254567	32542204	0,781633595	-0,422825589	
		0	FALSE					
SP55	T41	SP55T4	9	32567655	38397355	0,5	0,155713066	1
		TRUE						
SP55	T41	SP55T4	9	38453992	46912964	0,672	0,150401611	2
		FALSE						
SP55	T41	SP55T4	9	65973265	141015351	0,547	0,130465418	1
		FALSE						
SP55	T40	SP55T4	10	93816	46148326	0,747572559	-0,631943417	1
		TRUE						
SP55	T40	SP55T4	10	46272679	47667164	0,505	-0,707692251	0
		TRUE						
SP55	T41	SP55T4	10	47667380	71052083	0,744401956	-0,649951465	
		0	TRUE					
SP55	T40	SP55T4	10	71060418	71060707	0,576	-0,860398521	0
		TRUE						
SP55	T41	SP55T4	10	71098376	135279810	0,743985023	-0,652302877	
		0	TRUE					
SP55	T41	SP55T4	11	193096	134927578	0,505	-0,053576907	1
		TRUE						
SP55	T4	SP55T4	12	92252	133770096	0,5	-0,040313368	1
	TRUE							1
SP55	T41	SP55T4	13	19042705	115064542	0,574	-0,265298448	1
		FALSE						

SP55	T41	SP55T41 TRUE	14	19118067	107283160	0,505	-0,05279213	1
SP55	T41	SP55T41 TRUE	15	20433755	33446947	0,506	-0,097554667	1
SP55	T40	SP55T40 FALSE	15	33842260	50782335	0,609	-0,357889653	1
SP55	T41	SP55T41 TRUE	15	50782703	102388991	0,5	-0,051489242	1
SP55	T41	SP55T41 TRUE	16	215106	33372666	0,5	-0,0768927	1
SP55	T40	SP55T40 FALSE	16	33373381	33401997	0,722	0,006178503	2
SP55	T41	SP55T41 TRUE	16	33412679	90161231	0,503	-0,075964095	1
SP55	T41	SP55T41 TRUE	17	6115	18044893	0,506	-0,013576414	1
SP55	T41	SP55T41 TRUE	17	18057167	18291559	0,639	0,357643438	2
SP55	T41	SP55T41 TRUE	17	18301096	48186817	0,5	-0,021540438	1
SP55	T41	SP55T41 FALSE	17	48193233	81052423	0,572	0,158519427	2
SP55	T41	SP55T41 TRUE	18	166819	77927028	0,5	-0,033061488	1
SP55	T41	SP55T41 TRUE	19	311988	43922300	0,63	0,351151931	2
SP55	T41	SP55T41 TRUE	19	43999634	44515514	0,698	0,811456982	3
SP55	T41	SP55T41 TRUE	19	44535999	58806083	0,634	0,338638104	2
SP55	T41	SP55T41 TRUE	20	76962	62903729	0,5	-0,058926443	1
SP55	T41	SP55T41 TRUE	21	9907222	48080896	0,5	-0,066373161	1
SP55	T41	SP55T41 TRUE	22	16287789	51137094	0,5	-0,075268009	1
SP56	M2	SP56M2 TRUE	1	878314	59042001	0,5	-0,068906644	2
SP56	M0	SP56M0 FALSE	1	59096479	59096693	0,656	-0,204594582	2
SP56	M2	SP56M2 TRUE	1	59125683	248845458	0,5	0,079644049	2
SP56	M2	SP56M2 TRUE	2	173150	61191995	0,504	0,034053995	2
SP56	M0	SP56M0 TRUE	2	61235855	71351487	0,684	-0,439616103	2

SP56	M2	SP56M2	2	71357417	242836535	0,5055	0,063831106	2
SP56	M2	SP56M2	3	367757	197762623	0,5	0,058498523	2
SP56	M	SP56M	4	47658	190395259	0,5	0,072516371	2
SP56	M2	SP56M2	5	140532	73091228	0,5	0,044108135	2
SP56	M2	SP56M20	5	73144845	73339114	0,688214834	-0,478963146	
SP56	M2	SP56M2	5	73985121	180649486	0,503	0,06066904	2
SP56	M2	SP56M2	6	348051	170878886	0,5	0,046019825	2
SP56	M2	SP56M2	7	195501	80804928	0,609	0,340619785	4
SP56	M2	SP56M2	7	80805175	159053596	0,5	0,040076584	2
SP56	M2	SP56M2	8	191076	146222122	0,5	0,052178389	2
SP56	M0	SP56M	9	304478	19120752	0,697	-0,348007949	2
SP56	M0	SP56M	9	19619509	28889060	0,5	-1,033218966	0
SP56	M0	SP56M	9	29825106	66457267	0,69	-0,436102039	2
SP56	M2	SP56M2	9	66457388	141069927	0,5	0,01600415	2
SP56	M2	SP56M20	10	1018585	46280866	0,685311525	-0,4923352	
SP56	M1	SP56M	10	46963738	47087830	0,526	-0,41634425	1
SP56	M0	SP56M	10	47663227	51620231	0,6955	-0,336789911	2
SP56	M1	SP56M	10	51620278	51633027	0,515	-0,38503437	1
SP56	M0	SP56M	10	51785694	135381766	0,694	-0,450052002	2
SP56	M2	SP56M2	11	192997	134244123	0,5	0,066627307	2
SP56	M	SP56M	12	92252	133727843	0,5	0,030995632	2
SP56	M2	SP56M2	13	19042919	115064542	0,5	0,070359432	2
SP56	M0	SP56M	14	19117262	107198901	0,697	-0,418581271	2

SP56	M1	SP56M TRUE	15	20170449	20489310	0,6455	-0,046396119	3
SP56	M2	SP56M TRUE	15	21106528	33927764	0,503	0,106182567	2
SP56	M0	SP56M TRUE	15	33951910	40397936	0,6945	-0,409330144	2
SP56	M1	SP56M TRUE	15	40457431	40595627	0,5	-0,195061696	1
SP56	M0	SP56M FALSE	15	41101124	53809958	0,69	-0,434470145	2
SP56	M2	SP56M TRUE	15	53994493	102312835	0,5	0,016805053	2
SP56	M TRUE	SP56M	16	81779	15116400	0,5	-0,122950269	2 2
SP56	M2	SP56M 0 TRUE	16	15128416	28608341	0,679033208	-0,520834897	
SP56	M2	SP56M TRUE	16	28618037	31004812	0,512	-0,159826669	2
SP56	M0	SP56M TRUE	16	31044683	32046359	0,6825	-0,451276868	2
SP56	M0	SP56M TRUE	16	32190861	46391255	0,525	-0,827841218	0
SP56	M0	SP56M TRUE	16	46392238	46408060	0,5	-3,218652453	0
SP56	M2	SP56M TRUE	16	46408583	90161852	0,5	-0,078898699	2
SP56	M TRUE	SP56M	17	6115	5487164	0,505	-0,151425783	2 2
SP56	M0	SP56M TRUE	17	5629700	7095090	0,678	-0,386973074	2
SP56	M1	SP56M TRUE	17	7132192	7318935	0,519	-0,195277173	1
SP56	M1	SP56M 0 FALSE	17	7329632	7721231	0,640765823	-0,683335471	
SP56	M2	SP56M TRUE	17	7750010	22252214	0,504	-0,009575982	2
SP56	M0	SP56M TRUE	17	22253112	22261659	0,5	-3,955413518	0
SP56	M2	SP56M TRUE	17	25308788	81082463	0,503	-0,080727696	2
SP56	M2	SP56M TRUE	18	120645	15270908	0,511	0,02794999	2
SP56	M2	SP56M TRUE	18	18983766	77895192	0,5	0,069410592	2
SP56	M1	SP56M FALSE	19	335946	3645947	0,61	0,077780852	3

SP56	M1	SP56M	19	3653525	6713291	0,5	-0,274053918	1
		TRUE						
SP56	M1	SP56M	19	6718534	12958360	0,615	0,13538136	3
		FALSE						
SP56	M2	SP56M	19	12963143	15014719	0,507	-0,120298849	2
		TRUE						
SP56	M1	SP56M	19	15027433	24015602	0,602	0,182361747	3
		FALSE						
SP56	M2	SP56M	19	29567134	36164108	0,5	-0,116373865	2
		TRUE						
SP56	M2	SP56M	19	36164436	45873942	0,592	0,177741906	3
		FALSE						
SP56	M1	SP56M	19	45883554	47109011	0,515	-0,22224632	1
		TRUE						
SP56	M1	SP56M	19	47111663	50926126	0,616449179	-0,777828606	
		0 TRUE						
SP56	M2	SP56M	19	50962062	59082605	0,5	-0,073864345	2
		TRUE						
SP56	M	SP56M	20	76962	13939805	0,6	0,360152976	4
	TRUE							2
SP56	M2	SP56M	20	13971235	26113643	0,517	0,074348057	2
		TRUE						
SP56	M2	SP56M	20	29449353	37396262	0,616	0,319578465	4
		TRUE						
SP56	M4	SP56M	20	37524450	62737318	0,774716273	-0,010153961	
		0 FALSE						
SP56	M2	SP56M	21	9650104	14917605	0,528	-0,13202133	2
		TRUE						
SP56	M0	SP56M	21	15281853	15281957	0,5	-1,311321679	0
		TRUE						
SP56	M2	SP56M	21	15516898	48072916	0,5	-0,029651593	2
		TRUE						
SP56	M2	SP56M	22	16414200	51219006	0,5	-0,059063457	2
		TRUE						
SP56	S	SP56S	1	878314	1582202	0,505	-0,109310823	1
	TRUE							1
SP56	S0	SP56S	1	1582841	1583003	0,571409542	-0,264794927	2
		FALSE						
SP56	S	SP56S	1	1585597	248845458	0,5	-0,013205062	2
	TRUE							2
SP56	S	SP56S	2	173150	61191995	0,5	0,03177742	2
	TRUE							2
SP56	S	SP56S	2	61235855	71743984	0,58	-0,178682016	2
	TRUE							0
SP56	S	SP56S	2	71748088	242836535	0,5	0,019857889	2
	TRUE							2

SP56	S	SP56S	3	367757	197762623	0,505	0,018793478	2	2
TRUE									
SP56	S	SP56S	4	47658	49245009	0,503	-0,057259457	2	2
TRUE									
SP56	S	SP56S	4	52752812	58969622	0,608	0,496785202	7	3
TRUE									
SP56	S	SP56S	4	62445190	190395259	0,5	0,061980674	2	2
TRUE									
SP56	S	SP56S	5	140532	180649486	0,5	0,01680205	2	2
TRUE									
SP56	S	SP56S	6	348051	32497914	0,5	0,011008468	2	2
TRUE									
SP56	S	SP56S	6	32498033	32522408	0,689819192	0,20169538	6	
0	TRUE								
SP56	S	SP56S	6	32522464	170878886	0,504	0,047461982	2	2
TRUE									
SP56	S	SP56S	7	195501	80434918	0,561	0,15784537	4	2
TRUE									
SP56	S	SP56S	7	80804928	159053596	0,5	0,006370978	2	2
TRUE									
SP56	S	SP56S	8	191076	146222122	0,504	0,001955392	2	2
TRUE									
SP56	S	SP56S	9	304478	27296705	0,558	-0,25550545	1	0
FALSE									
SP56	S	SP56S	9	27330514	66457388	0,646	0,008386662	4	0
TRUE									
SP56	S	SP56S	9	66457475	141069927	0,5	-0,097830276	2	2
TRUE									
SP56	S	SP56S	10	1018585	38737254	0,571861072	-0,263274216	2	
0	FALSE								
SP56	S	SP56S	10	42680864	135381766	0,579	-0,23209867	2	0
TRUE									
SP56	S	SP56S	11	192997	134244123	0,5	0,011031422	2	2
TRUE									
SP56	S	SP56S	12	92252	133727843	0,5	-0,01107203	2	2
TRUE									
SP56	S	SP56S	13	19042919	115064542	0,5	0,017956368	2	2
TRUE									
SP56	S	SP56S	14	19117262	107198901	0,5	-0,010729564	2	2
TRUE									
SP56	S	SP56S	15	20170449	34115088	0,587788726	-0,208579161	2	
0	TRUE								
SP56	S	SP56S	15	34517466	102312835	0,5	-0,051013083	2	2
TRUE									
SP56	S	SP56S	16	81779	28608341	0,5	-0,079465845	2	2
TRUE									
SP56	S	SP56S	16	28618037	28618071	0,671598058	0,119342145	5	
0	TRUE								

SP56	S	SP56S	16	29790709	34274796	0,521	-0,129945442	2	1	FALSE
SP56	S	SP56S	16	46388407	46427047	0,5	-2,667808341	0	0	TRUE
SP56	S	SP56S	16	46602819	90161852	0,5	-0,054171574	2	2	TRUE
SP56	S	SP56S	17	6115	22214959	0,5	-0,101359672	2	2	TRUE
SP56	S	SP56S	17	22252214	22261659	0,5	-2,818521981	0	0	TRUE
SP56	S	SP56S	17	25308788	81082463	0,504	-0,074759473	2	2	TRUE
SP56	S	SP56S	18	120645	15270908	0,503	-0,008253365	2	2	TRUE
SP56	S	SP56S	18	18983766	77895192	0,5095	0,028902501	2	2	TRUE
SP56	S	SP56S	19	335946	24015602	0,551	0,007891943	3	2	FALSE
SP56	S	SP56S	19	29567134	36003430	0,5	-0,151533819	1	1	TRUE
SP56	S	SP56S	19	36015491	51191003	0,6	0,049126598	4	1	TRUE
SP56	S	SP56S	19	51191172	59082605	0,5	-0,079778904	2	2	TRUE
SP56	S	SP56S	20	76962	26113643	0,557	0,027265302	3	1	FALSE
SP56	S	SP56S	20	29449353	37396262	0,592	0,036523836	4	1	TRUE
SP56	S	SP56S	20	37524450	62737318	0,629350068	-0,055252446	3	0	FALSE
SP56	S	SP56S	21	9650104	11181645	0,575	-0,001985504	3	1	TRUE
SP56	S	SP56S	21	14433036	48072916	0,5	-0,043937336	2	2	TRUE
SP56	S	SP56S	22	16414200	51219006	0,5	-0,073080743	2	2	TRUE
SP56	T1	SP56T1	1	878314	59042001	0,5	-0,051421671	2	2	TRUE
SP56	T1	SP56T1	1	59096479	59096693	0,712	-0,069136526	3	1	FALSE
SP56	T1	SP56T1	1	59125683	248845458	0,5	0,039428341	2	2	TRUE
SP56	T1	SP56T1	2	173150	61191995	0,503	0,183643649	2	2	TRUE
SP56	T1	SP56T1	2	61235855	71351487	0,764044023	-0,387090095	3	0	FALSE

SP56	T12	SP56T12	FALSE	2	71357417	242836535	0,556	0,106574932	3
SP56	T12	SP56T12	TRUE	3	367757	197762623	0,5	0,121381503	2
SP56	T13	SP56T13	TRUE	4	47658	49245009	0,5	-0,184614493	2	2
SP56	T13	SP56T13	TRUE	4	52752812	58969622	0,904	2,781614915	38
SP56	T12	SP56T12	FALSE	4	62445190	140640703	0,512	-0,127408644	2
SP56	T12	SP56T12	FALSE	4	140810637	149358014	0,6585	0,239271171	4
SP56	T11	SP56T11	FALSE	4	151141918	190395259	0,553	-0,135370528	2
SP56	T12	SP56T12	TRUE	5	140532	73091228	0,506	0,069086485	2
SP56	T11	SP56T110	FALSE	5	73144845	73339114	0,687833344	-0,790888825	
SP56	T12	SP56T12	TRUE	5	73985121	180649486	0,5	-0,033657663	2
SP56	T12	SP56T12	TRUE	6	348051	32497914	0,5	-0,002005537	2
SP56	T10	SP56T10	TRUE	6	32498033	32521233	0,739	-0,367703928	2
SP56	T12	SP56T12	TRUE	6	32522397	170878886	0,506	0,025843295	2
SP56	T12	SP56T12	TRUE	7	195501	80805263	0,623	0,377827749	4
SP56	T12	SP56T12	TRUE	7	80805381	159053596	0,5	0,005220108	2
SP56	T12	SP56T12	TRUE	8	191076	146222122	0,5	-0,008884666	2
SP56	T12	SP56T120	TRUE	9	304478	19087154	0,742154623	-0,515078558	
SP56	T10	SP56T10	TRUE	9	19119737	28889060	0,509	-1,397341848	0
SP56	T15	SP56T150	TRUE	9	29825106	44175535	0,843014671	0,200797884	
SP56	T12	SP56T12	FALSE	9	45372291	69002200	0,601	0,001306755	3
SP56	T10	SP56T10	FALSE	9	69002538	135930735	0,764	-0,398923039	3
SP56	T11	SP56T11	TRUE	9	135937248	135962585	0,516	-0,487826261	1
SP56	T10	SP56T10	FALSE	9	135974100	141069927	0,745	-0,43579703	2

SP56	T12	SP56T10	TRUE	10	1018585	46147545	0,72681921	-0,598428419
SP56	T11	SP56T11	TRUE	10	46148266	47087830	0,509	-0,535982569 1
SP56	T10	SP56T10	TRUE	10	47663227	51592744	0,747	-0,486204291 2
SP56	T11	SP56T11	FALSE	10	51620231	51633027	0,525	-0,361826628 1
SP56	T12	SP56T10	TRUE	10	51785694	135381766	0,736709649	-0,545227031
SP56	T12	SP56T11	TRUE	11	192997	134244123	0,504	-0,016189662 2
SP56	T12	SP56T11	TRUE	12	92252	133727843	0,505	0,069842926 2 2
SP56	T12	SP56T11	TRUE	13	19042919	115064542	0,5	-0,004036919 2
SP56	T12	SP56T11	TRUE	14	19117262	107198901	0,5	-0,004051697 2
SP56	T11	SP56T11	TRUE	15	20170449	22383189	0,588	-0,283208635 2
SP56	T12	SP56T10	TRUE	15	22466002	38857631	0,736496008	-0,546397199
SP56	T12	SP56T11	TRUE	15	40030440	102312835	0,5	-0,034607368 2
SP56	T12	SP56T11	TRUE	16	81779	34274796	0,5	0,014913975 2 2
SP56	T10	SP56T10	TRUE	16	46388407	46394424	0,5	-3,063275624 0
SP56	T10	SP56T10	TRUE	16	46394533	46408060	0,5	-3,137730647 0
SP56	T10	SP56T10	TRUE	16	46408583	46427047	0,5	-3,099348895 0
SP56	T12	SP56T11	TRUE	16	46602819	90161852	0,5	0,031910166 2
SP56	T12	SP56T11	TRUE	17	6115	5487164	0,5	-0,125437706 2 2
SP56	T12	SP56T10	TRUE	17	5629700	6546259	0,714586056	-0,661628202
SP56	T12	SP56T11	TRUE	17	6553583	6561192	0,533	-0,012390655 2
SP56	T12	SP56T10	TRUE	17	6562141	7132192	0,735899874	-0,54965737
SP56	T12	SP56T11	TRUE	17	7133609	7318935	0,5	0,017994837 2
SP56	T12	SP56T10	TRUE	17	7329632	7721231	0,704129567	-0,713537914

SP56	T12	SP56T1 TRUE	17	7750010	22252214	0,502	-0,048725682	2
SP56	T11000	SP56T10 TRUE	17	22253112	22253231	0,998864912	-4,105997203	
SP56	T12	SP56T1 TRUE	17	25308788	34813271	0,512	-0,030621035	2
SP56	T11	SP56T1 FALSE	17	34842521	37009072	0,648	-0,501198888	2
SP56	T12	SP56T1 TRUE	17	37075042	81082463	0,506	-0,06415496	2
SP56	T12	SP56T1 TRUE	18	120645	15270908	0,505	-0,051689838	2
SP56	T12	SP56T1 TRUE	18	18983766	77895192	0,5	0,010109658	2
SP56	T12	SP56T1 FALSE	19	335946	3452683	0,649	0,261536512	4
SP56	T12	SP56T1 TRUE	19	3527110	6679511	0,5	-0,096633425	2
SP56	T12	SP56T1 FALSE	19	6679563	12985576	0,647	0,33389991	4
SP56	T12	SP56T1 TRUE	19	13220703	15014719	0,5	0,004515854	2
SP56	T12	SP56T1 FALSE	19	15027433	30314459	0,633	0,333016998	4
SP56	T12	SP56T1 TRUE	19	31038995	36045772	0,5	-0,112586868	2
SP56	T12	SP56T1 TRUE	19	36142296	40901011	0,716	0,719554716	7
SP56	T12	SP56T1 TRUE	19	40904602	41387907	0,655	0,526807042	5
SP56	T12	SP56T1 FALSE	19	41397370	41532133	0,748	0,807652305	7
SP56	T12	SP56T1 TRUE	19	41533112	44012880	0,663	0,536273196	5
SP56	T12	SP56T1 TRUE	19	44047550	46142053	0,72	0,800493823	7
SP56	T12	SP56T1 TRUE	19	46216642	47028898	0,509	-0,147459075	2
SP56	T12	SP56T10 TRUE	19	47109011	50926126	0,701773953	-0,72497865	
SP56	T12	SP56T1 TRUE	19	50962062	59082605	0,5	-0,087112231	2
SP56	T1TRUE	SP56T1	20	76962	14066276	0,817	-0,002506505	4 0
SP56	T10	SP56T1 TRUE	20	14306953	29625720	0,7375	-0,503455064	2

SP56	T12	SP56T1 TRUE	20	29625788	29652000	0,518	-0,000522438	2
SP56	T14	SP56T10 TRUE	20	29873577	62737318	0,816037214	-0,027986329	
SP56	T11	SP56T1 TRUE	21	9650104	11181645	0,614	-0,172139528	2
SP56	T12	SP56T1 TRUE	21	14433036	48072916	0,5	-0,063814308	2
SP56	T12	SP56T1 TRUE	22	16414200	51219006	0,5	-0,064062728	2
SP56	T22	SP56T2 TRUE	1	878314	59042001	0,5	0,006042429	2
SP56	T23	SP56T20 TRUE	1	59096479	59096693	0,574185241	-0,056202373	
SP56	T22	SP56T2 TRUE	1	59125683	248845458	0,5	0,026453954	2
SP56	T22	SP56T2 TRUE	2	173150	242836535	0,5	0,024021096	2
SP56	T22	SP56T2 TRUE	3	367757	197762623	0,5	0,037571872	2
SP56	T2 TRUE	SP56T2	4	47658	190395259	0,5	0,033707541	2 2
SP56	T22	SP56T2 TRUE	5	140532	180649486	0,5	0,008579241	2
SP56	T22	SP56T2 TRUE	6	348051	32498033	0,5	0,028981362	2
SP56	T26	SP56T20 TRUE	6	32521022	32521179	0,619079548	0,104533831	
SP56	T22	SP56T2 TRUE	6	32521230	170878886	0,503	0,015328094	2
SP56	T22	SP56T2 TRUE	7	195501	57642490	0,545	0,139078472	4
SP56	T21	SP56T2 TRUE	7	62669789	76916010	0,5695	0,053377805	4
SP56	T22	SP56T2 TRUE	7	76916046	159053596	0,5	0,017340946	2
SP56	T22	SP56T2 TRUE	8	191076	146222122	0,5	0,022293244	2
SP56	T21	SP56T2 TRUE	9	304478	29825925	0,505	-0,147393137	1
SP56	T25	SP56T20 TRUE	9	31254567	69777408	0,611585231	0,076425524	
SP56	T21	SP56T2 TRUE	9	69846339	140638416	0,521	-0,06335198	2
SP56	T21	SP56T2 TRUE	9	140648742	141069927	0,531	-0,068843023	2

SP56	T20	SP56T2 FALSE	10	1018585	135381766	0,54	-0,120610134	2
SP56	T22	SP56T2 TRUE	11	192997	134244123	0,5	0,046231497	2
SP56	T2TRUE	SP56T2	12	92252	133727843	0,5	0,015633923	2
SP56	T22	SP56T2 TRUE	13	19042919	115064542	0,502	0,012230628	2
SP56	T22	SP56T2 TRUE	14	19117262	107198901	0,5	0,043653321	2
SP56	T24	SP56T2 0 TRUE	15	20170449	20446256	0,581885042	-0,029876074	
SP56	T22	SP56T2 TRUE	15	20447987	102312835	0,5	-0,007797829	2
SP56	T2TRUE	SP56T2	16	81779	34274796	0,5	-0,01768108	2
SP56	T20	SP56T2 TRUE	16	46388407	46405410	0,5	-3,255172873	0
SP56	T21000	SP56T2 0 TRUE	16	46405874	46406598	0,991149399	-4,223973733	
SP56	T22	SP56T2 TRUE	16	46407745	90161852	0,5	-0,055669213	2
SP56	T2TRUE	SP56T2	17	6115	22214959	0,5	-0,037516669	2
SP56	T21000	SP56T2 0 TRUE	17	22252214	22253128	0,991149399	-3,597716328	
SP56	T20	SP56T2 TRUE	17	22253134	22261659	0,5	-3,427599568	0
SP56	T22	SP56T2 TRUE	17	25308788	81082463	0,503	-0,013665231	2
SP56	T22	SP56T2 TRUE	18	120645	15270908	0,507	-0,053132353	2
SP56	T22	SP56T2 TRUE	18	18983766	77895192	0,504	0,009021151	2
SP56	T22	SP56T2 TRUE	19	335946	36044524	0,5	0,017050017	2
SP56	T21	SP56T2 TRUE	19	36045772	50662529	0,5765	0,070178493	5
SP56	T22	SP56T2 TRUE	19	50662726	59082605	0,5	-0,042838869	2
SP56	T2TRUE	SP56T2	20	76962	13912309	0,592	0,060041297	4 0
SP56	T21	SP56T2 FALSE	20	13939805	26113643	0,512	-0,070910548	1
SP56	T20	SP56T2 TRUE	20	29449353	62737318	0,6055	0,087683774	5

SP56	T22	SP56T220 TRUE	21	9650104	11181645	0,541961639	-0,161444847	
SP56	T22	SP56T22 TRUE	21	14433036	48072916	0,5	0,004427208	2
SP56	T22	SP56T22 TRUE	22	16414200	51219006	0,5	0,002745821	2
SP56	T32	SP56T3 TRUE	1	878314	59042001	0,5	-0,097883576	2
SP56	T30	SP56T3 TRUE	1	59096479	59096693	0,694	-0,011764672	3
SP56	T32	SP56T3 TRUE	1	59125683	248845458	0,5	0,038502276	2
SP56	T32	SP56T3 TRUE	2	173150	61191995	0,5	0,149958573	2
SP56	T30	SP56T3 FALSE	2	61235855	71357417	0,679	-0,2602233	2
SP56	T32	SP56T3 TRUE	2	71360282	242836535	0,5	0,097625253	2
SP56	T32	SP56T3 TRUE	3	367757	197762623	0,505	0,102385759	2
SP56	T3 TRUE	SP56T3	4	47658	49245009	0,5	-0,106760163	2 2
SP56	T32	SP56T3 TRUE	4	52752812	58969622	0,904	2,337125696	37
SP56	T32	SP56T3 TRUE	4	62445190	190395259	0,5	-0,028727871	2
SP56	T32	SP56T3 TRUE	5	140532	43609343	0,504	0,07383469	2
SP56	T32	SP56T3 TRUE	5	49929151	150322270	0,5	0,053917236	2
SP56	T30	SP56T3 TRUE	5	150400587	150407783	0,5	-1,073619707	0
SP56	T32	SP56T3 TRUE	5	150409477	180649486	0,5	-0,066087759	2
SP56	T32	SP56T3 TRUE	6	348051	170878886	0,5	0,004326134	2
SP56	T32	SP56T3 TRUE	7	195501	80805518	0,596	0,262958369	4
SP56	T32	SP56T3 TRUE	7	81372156	159053596	0,503	-0,027696524	2
SP56	T32	SP56T3 TRUE	8	191076	146222122	0,5	-0,008165142	2
SP56	T30	SP56T3 TRUE	9	304478	19705432	0,649	-0,364134525	2
SP56	T30	SP56T3 FALSE	9	20620575	28889060	0,514	-0,769680372	0

SP56	T35	SP56T30	9	29825106	45372357	0,760858019	0,137119414	TRUE
SP56	T32	SP56T3	9	65973265	69002538	0,509	0,147888735	2 TRUE
SP56	T33	SP56T30	9	69120693	141069927	0,680319927	-0,281641991	FALSE
SP56	T32	SP56T30	10	1018585	46224381	0,64502211	-0,432742344	TRUE
SP56	T31	SP56T3	10	46280866	47087830	0,519	-0,418833786	1 TRUE
SP56	T30	SP56T3	10	47663227	135381766	0,652	-0,392826362	2 TRUE
SP56	T32	SP56T3	11	192997	134244123	0,5	-0,002497294	2 TRUE
SP56	T3	SP56T3	12	92252	133727843	0,509	0,06179708	2 2 TRUE
SP56	T32	SP56T3	13	19042919	115064542	0,5	0,015298517	2 TRUE
SP56	T32	SP56T3	14	19117262	107198901	0,508	0,006475367	2 TRUE
SP56	T31	SP56T3	15	20170449	22383189	0,506	-0,312216975	1 TRUE
SP56	T32	SP56T30	15	22466002	38857631	0,65287657	-0,40046192	TRUE
SP56	T32	SP56T3	15	40030440	102312835	0,5	-0,021316859	2 TRUE
SP56	T3	SP56T3	16	81779	34274796	0,5	-0,045717151	2 2 TRUE
SP56	T30	SP56T3	16	46388407	46408060	0,5	-4,340230915	0 TRUE
SP56	T32	SP56T3	16	46408583	90161852	0,5	-0,01758899	2 TRUE
SP56	T3	SP56T3	17	6115	5485367	0,506	-0,17953903	2 2 TRUE
SP56	T30	SP56T3	17	5487164	7132192	0,652	-0,308424742	2 TRUE
SP56	T32	SP56T3	17	7133609	22066914	0,5	-0,083832072	2 TRUE
SP56	T30	SP56T3	17	22214959	22253121	0,5	-3,762807151	0 TRUE
SP56	T32	SP56T3	17	22253128	81082463	0,5	-0,121608392	2 TRUE
SP56	T32	SP56T3	18	120645	77895192	0,505	-0,004242314	2 TRUE
SP56	T31	SP56T3	19	335946	3534696	0,628	0,154427144	4 FALSE

SP56	T32	SP56T3 TRUE	19	3538654	6896344	0,506	-0,175941289	2
SP56	T31	SP56T3 TRUE	19	7129086	8321182	0,619	0,10109525	3
SP56	T35	SP56T30 TRUE	19	8321937	8326999	0,767785767	0,179530425	
SP56	T32	SP56T3 FALSE	19	8402599	12975608	0,615	0,199668343	4
SP56	T32	SP56T3 TRUE	19	12985576	14992042	0,508	-0,073317959	2
SP56	T32	SP56T3 FALSE	19	14997907	24015602	0,613	0,184218423	4
SP56	T32	SP56T3 TRUE	19	29567134	30156601	0,6725	0,495085205	6
SP56	T32	SP56T3 TRUE	19	30156797	36045772	0,5	-0,183709793	2
SP56	T32	SP56T3 FALSE	19	36142296	40929363	0,686	0,492840559	6
SP56	T32	SP56T3 TRUE	19	40947448	44047550	0,6455	0,357843201	5
SP56	T31	SP56T3 FALSE	19	44049881	45924692	0,696	0,535289758	6
SP56	T31	SP56T3 TRUE	19	46057081	47137459	0,513	-0,205838004	1
SP56	T31	SP56T30 TRUE	19	47137972	50779151	0,591341052	-0,635910499	
SP56	T32	SP56T3 TRUE	19	50863275	59082605	0,504	-0,169276834	2
SP56	T3 TRUE	SP56T3	20	76962	13912309	0,739	0,01459706	4 0
SP56	T30	SP56T3 TRUE	20	13939805	29625720	0,643	-0,354752186	2
SP56	T33	SP56T3 TRUE	20	29625788	29652000	0,509	0,170367398	3
SP56	T34	SP56T30 FALSE	20	29873577	62737318	0,725245044	-0,06315868	
SP56	T32	SP56T3 TRUE	21	9650104	48072916	0,5	-0,050435417	2
SP56	T32	SP56T3 TRUE	22	16414200	51219006	0,5	-0,095393832	2
SP56	T42	SP56T4 TRUE	1	878314	59042001	0,5	0,012010435	2
SP56	T41	SP56T4 TRUE	1	59096479	59096689	0,686	0,192412207	3
SP56	T42	SP56T4 TRUE	1	59096693	248845458	0,5	0,032359123	2

SP56	T41	SP56T4 FALSE	2	173150	61191995	0,556	0,022977083	2
SP56	T40	SP56T4 TRUE	2	61235855	71351487	0,81	-0,485503587	2
SP56	T42	SP56T4 TRUE	2	71357417	242836535	0,5	0,157877008	2
SP56	T42	SP56T4 TRUE	3	367757	197762623	0,5	0,156948149	2
SP56	T4 FALSE	SP56T4	4	47658	49245009	0,541	-0,037340624	2
SP56	T42	SP56T4 TRUE	4	52752812	139482765	0,5	0,057909801	2
SP56	T42	SP56T4 TRUE	4	140616462	144940333	0,7765	1,341076981	9
SP56	T42	SP56T4 TRUE	4	145020647	146016997	0,529	0,044690085	2
SP56	T42	SP56T4 TRUE	4	146048554	149358014	0,7855	1,225788418	9
SP56	T42	SP56T4 TRUE	4	151141918	190395259	0,571	0,232398509	3
SP56	T42	SP56T4 TRUE	5	140532	43609343	0,5	-0,105090706	2
SP56	T41	SP56T4 FALSE	5	49929151	73091228	0,566	-0,292385118	1
SP56	T410	SP56T4 TRUE	5	73144845	73207372	0,759646987	-0,938758123	
SP56	T41	SP56T4 FALSE	5	73339114	180649486	0,598	-0,146174721	2
SP56	T42	SP56T4 TRUE	6	348051	170878886	0,5	0,035770274	2
SP56	T42	SP56T4 FALSE	7	195501	80805518	0,649	0,482208445	4
SP56	T42	SP56T4 TRUE	7	81372156	159053596	0,5	0,027601695	2
SP56	T42	SP56T4 TRUE	8	191076	42865753	0,5	0,019906548	2
SP56	T410	SP56T4 TRUE	8	43172409	46849355	0,679795529	-1,352596687	
SP56	T42	SP56T4 TRUE	8	48033794	146222122	0,5	0,010237947	2
SP56	T40	SP56T4 TRUE	9	304478	19120752	0,8035	-0,617789489	2
SP56	T40	SP56T4 TRUE	9	19619509	28889060	0,5	-1,975793707	0
SP56	T40	SP56T4 TRUE	9	29825106	44175535	0,8885	0,186212907	4

SP56	T41	SP56T4 FALSE	9	45372291	69002538	0,636	0,071138766	3
SP56	T40	SP56T4 FALSE	9	69120693	135930735	0,816	-0,511669423	2
SP56	T42	SP56T4 TRUE	9	135937248	135962585	0,516	-0,051171086	2
SP56	T40	SP56T4 TRUE	9	135974100	141069927	0,815	-0,516510955	2
SP56	T40	SP56T4 FALSE	10	1018585	46280866	0,816	-0,563241202	2
SP56	T41	SP56T4 TRUE	10	46963738	47087830	0,505	-0,419860669	1
SP56	T40	SP56T4 TRUE	10	47663227	51620317	0,814	-0,47853921	2
SP56	T41	SP56T4 TRUE	10	51620499	51633027	0,522	-0,902109307	1
SP56	T42	SP56T4 0 FALSE	10	51785694	135381766	0,817870903	-0,538564661	
SP56	T42	SP56T4 TRUE	11	192997	102398729	0,5	-0,119958337	2
SP56	T42	SP56T4 FALSE	11	102464451	134244123	0,567	0,4370437	3
SP56	T4 TRUE	SP56T4	12	92252	133727843	0,505	0,13522794	2 2
SP56	T42	SP56T4 TRUE	13	19042919	115064542	0,5	-0,077342875	2
SP56	T42	SP56T4 TRUE	14	19117262	23389796	0,502	0,031340034	2
SP56	T40	SP56T4 TRUE	14	23394007	23467664	0,721	-0,431545587	2
SP56	T42	SP56T4 TRUE	14	23504021	107198901	0,5	0,020739917	2
SP56	T41	SP56T4 TRUE	15	20170449	22383189	0,5815	-0,600777928	2
SP56	T40	SP56T4 FALSE	15	22466002	38857631	0,744	-0,966717225	1
SP56	T41	SP56T4 FALSE	15	40030440	102312835	0,583	-0,147730079	2
SP56	T4 TRUE	SP56T4	16	81779	34274796	0,5	0,008071807	2 2
SP56	T40	SP56T4 TRUE	16	46388407	46393052	0,5	-3,361406354	0
SP56	T41000	SP56T4 0 TRUE	16	46393218	46394221	0,999351491	-4,370109042	
SP56	T40	SP56T4 TRUE	16	46394410	46405874	0,5	-4,120399881	0

SP56	T40	SP56T40 TRUE	16	46406219	46408610	0,5	-4,164324378	0
SP56	T42	SP56T42 TRUE	16	46427047	90161852	0,5	-0,015552545	2
SP56	T42	SP56T42 FALSE	17	6115	5487164	0,514	-0,033615801	2
SP56	T40	SP56T40 FALSE	17	5629700	6546259	0,756	-0,780040335	1
SP56	T42	SP56T42 TRUE	17	6553583	6560977	0,511	0,071914935	2
SP56	T40	SP56T40 TRUE	17	6561192	7132192	0,72	-0,467786574	2
SP56	T42	SP56T42 TRUE	17	7133609	7318935	0,511	-0,04144656	2
SP56	T420	SP56T420 TRUE	17	7329632	7721231	0,772853349	-0,857227271	
SP56	T42	SP56T42 TRUE	17	7750010	22252214	0,504	-0,0395951	2
SP56	T40	SP56T40 TRUE	17	22253112	22261659	0,5	-3,696815315	0
SP56	T42	SP56T42 TRUE	17	25308788	81082463	0,5	-0,038436975	2
SP56	T41	SP56T41 FALSE	18	120645	15270908	0,589	-0,240918821	2
SP56	T42	SP56T42 FALSE	18	18983766	77895192	0,515	0,056361561	2
SP56	T42	SP56T42 TRUE	19	335946	3645947	0,645	0,492385515	4
SP56	T42	SP56T42 TRUE	19	3653525	6478925	0,505	0,106092456	2
SP56	T42	SP56T42 FALSE	19	6677989	12985576	0,656	0,54081831	4
SP56	T42	SP56T42 TRUE	19	13220703	14997907	0,5	0,137826043	2
SP56	T42	SP56T42 FALSE	19	15014719	30314459	0,6545	0,541491604	4
SP56	T42	SP56T42 TRUE	19	31038995	36038390	0,506	0,029720757	2
SP56	T42	SP56T42 FALSE	19	36044524	40327312	0,729	0,920022514	6
SP56	T42	SP56T42 TRUE	19	40328327	44047550	0,681	0,727002906	5
SP56	T42	SP56T42 FALSE	19	44049881	46142053	0,726	0,885082975	6
SP56	T42	SP56T42 TRUE	19	46216642	47028898	0,504	0,04857534	2

SP56	T42	SP56T40	19	47109011	50863275	0,798583594	-0,683784435	TRUE
SP56	T42	SP56T4TRUE	19	50926126	59082605	0,5	0,00223831	2
SP56	T4TRUE	SP56T4	20	76962	14066276	0,88	0,181930654	4 0
SP56	T40	SP56T4TRUE	20	14306953	29625701	0,8155	-0,423564238	2
SP56	T43	SP56T4TRUE	20	29625716	29633986	0,507	0,371026426	3
SP56	T40	SP56T4TRUE	20	29652000	62737318	0,8875	0,180741333	4
SP56	T41	SP56T4TRUE	21	9650104	10807898	0,76	-0,183092248	3
SP56	T42	SP56T4TRUE	21	10825608	14917605	0,523	-0,201486714	2
SP56	T40	SP56T4TRUE	21	15281853	15516898	0,7305	-0,536803328	2
SP56	T42	SP56T4TRUE	21	15516948	48072916	0,5	-0,180808195	2
SP56	T42	SP56T4TRUE	22	16414200	51219006	0,5	0,038857687	2
SP57	M1	SP57MTRUE	1	900298	249212725	0,5	-0,006602941	1
SP57	M1	SP57MTRUE	2	173150	242946289	0,505	-0,004135949	1
SP57	M1	SP57MTRUE	3	403690	197762623	0,5	0,011521216	1
SP57	MTRUE	SP57M	4	60400	190904031	0,507	0,013605923	1 1
SP57	M1	SP57MTRUE	5	163266	180687212	0,502	-0,005571713	1
SP57	M1	SP57MTRUE	6	203878	170892848	0,5	0,02141131	1
SP57	M1	SP57MTRUE	7	286534	100608573	0,5	-0,001332391	1
SP57	M0	SP57MFALSE	7	100615449	100615533	0,697	-0,274980582	1
SP57	M1	SP57MTRUE	7	100624718	159025494	0,5	-0,00145041	1
SP57	M1	SP57MTRUE	8	250564	146115367	0,501	-0,001831409	1
SP57	M1	SP57MTRUE	9	117713	45372357	0,5	-0,009196665	1
SP57	M0	SP57MFALSE	9	65617649	65973595	0,726	-0,16778481	1

SP57	M1	SP57M TRUE	9	66455566	141069978	0,5	-0,005136135	1
SP57	M1	SP57M TRUE	10	412449	135183608	0,5	-0,0188709	1
SP57	M1	SP57M TRUE	11	193112	134856661	0,5	0,010000322	1
SP57	M1	SP57M TRUE	12	247900	133303973	0,5	-0,015100017	1
SP57	M1	SP57M TRUE	12	133304146	133304174	0,75	0,078456479	2
SP57	M1	SP57M TRUE	12	133304891	133463969	0,508	-0,13170389	1
SP57	M1	SP57M TRUE	13	19059494	115064685	0,505	0,008947972	1
SP57	M1	SP57M TRUE	14	19118067	107183367	0,504	0,000564235	1
SP57	M1	SP57M FALSE	15	20170150	22148395	0,6	-0,005792966	1
SP57	M1	SP57M TRUE	15	22319166	102004231	0,5	-0,005068471	1
SP57	M1	SP57M TRUE	16	240280	90162340	0,5	-0,049366925	1
SP57	M TRUE	SP57M	17	6115	81082365	0,504	-0,033324813	1 1
SP57	M1	SP57M TRUE	18	348161	77895192	0,5	0,011374211	1
SP57	M1	SP57M TRUE	19	335946	59074653	0,5	-0,065305478	1
SP57	M1	SP57M TRUE	20	138125	62899394	0,5	-0,004365777	1
SP57	M1	SP57M TRUE	21	9891930	10807706	0,6835	0,271468628	2
SP57	M1	SP57M TRUE	21	10825620	48083526	0,5	-0,011921535	1
SP57	M1	SP57M TRUE	22	16255826	51182485	0,5	-0,043910346	1
SP57	S TRUE	SP57S	1	900298	121124514	0,5	-0,033417626	1 1
SP57	S TRUE	SP57S	1	142620901	144854497	0,653	0,344373424	2 1
SP57	S TRUE	SP57S	1	144854597	249212725	0,5	0,004695721	1 1
SP57	S TRUE	SP57S	2	173150	242946289	0,5	-0,002307533	1 1
SP57	S TRUE	SP57S	3	403690	197762623	0,5	0,00852788	1 1

SP57	S	SP57S	4	60400	190904031	0,5	0,018808531	1	1	TRUE
SP57	S	SP57S	5	163266	180687212	0,5	-0,005663628	1	1	TRUE
SP57	S	SP57S	6	203878	32975869	0,51	0,009228945	1	1	FALSE
SP57	S	SP57S	6	33022307	33022368	0,733	0,083444251	2	1	FALSE
SP57	S	SP57S	6	33047432	170892848	0,503	0,015193598	1	1	TRUE
SP57	S	SP57S	7	286534	5167408	0,5	-0,119371136	1	1	TRUE
SP57	S	SP57S	7	5172208	5172295	0,833	-0,777646358	1	0	TRUE
SP57	S	SP57S	7	5239139	100608573	0,5	0,031467974	1	1	TRUE
SP57	S	SP57S	7	100615449	100615533	0,7	0,032676385	2	1	FALSE
SP57	S	SP57S	7	100624718	159025494	0,5	0,015173959	1	1	TRUE
SP57	S	SP57S	8	250564	146115367	0,5	-0,007176935	1	1	TRUE
SP57	S	SP57S	9	117713	45372357	0,5	-0,012983404	1	1	TRUE
SP57	S	SP57S	9	65617649	70731810	0,61	-0,014520267	1	1	FALSE
SP57	S	SP57S	9	71224796	141069978	0,5	0,003600114	1	1	TRUE
SP57	S	SP57S	10	412449	135183608	0,503	-0,048530691	1	1	TRUE
SP57	S	SP57S	11	193112	18267135	0,5065	0,024076427	1	1	TRUE
SP57	S	SP57S	11	18267353	18267373	0,828	0,040179809	2	1	TRUE
SP57	S	SP57S	11	18267431	134856661	0,504	0,004687684	1	1	TRUE
SP57	S	SP57S	12	247900	133463969	0,5	-0,031725055	1	1	TRUE
SP57	S	SP57S	13	19059494	19960034	0,515	-0,092810986	1	1	TRUE
SP57	S	SP57S	13	19962045	20625876	0,714	-0,500346406	1	0	FALSE
SP57	S	SP57S	13	21535586	115064685	0,508	0,011468901	1	1	TRUE
SP57	S	SP57S	14	19118067	107183367	0,5	-0,008099383	1	1	TRUE

SP57	S	SP57S	15	20170150	20874667	0,5955	-0,12643898	1	1	FALSE
SP57	S	SP57S	15	20874676	102004231	0,5	-0,01208655	1	1	TRUE
SP57	S	SP57S	16	240280	90162340	0,503	-0,070627831	1	1	TRUE
SP57	S	SP57S	17	6115	81082365	0,5	-0,057563814	1	1	TRUE
SP57	S	SP57S	18	348161	77895192	0,5	0,012348781	1	1	TRUE
SP57	S	SP57S	19	335946	59074653	0,5	-0,134568931	1	1	TRUE
SP57	S	SP57S	20	138125	62899394	0,506	0,006765468	1	1	TRUE
SP57	S	SP57S	21	9891930	48083526	0,5	-0,054584649	1	1	TRUE
SP57	S	SP57S	22	16255826	51182485	0,5	-0,091581101	1	1	TRUE
SP57	T1	SP57T1	1	900298	249212725	0,5	-0,020001498	1	1	TRUE
SP57	T1	SP57T1	2	173150	242946289	0,5	-0,030387477	1	1	TRUE
SP57	T1	SP57T1	3	403690	197762623	0,5	-0,008359566	1	1	TRUE
SP57	T1	SP57T1	4	60400	190904031	0,5	-0,0052765	1	1	TRUE
SP57	T1	SP57T1	5	163266	180687212	0,5	-0,031328723	1	1	TRUE
SP57	T1	SP57T1	6	203878	57472533	0,5045	-0,005835225	1	1	TRUE
SP57	T1	SP57T1	6	62687960	170892848	0,502	-0,012637114	1	1	TRUE
SP57	T1	SP57T1	7	286534	100608573	0,5	0,153058194	2	2	TRUE
SP57	T1	SP57T1	7	100615449	100615533	0,559156504	-0,235456019	1	0	TRUE
SP57	T1	SP57T1	7	100624718	159025494	0,545	0,13024891	2	1	TRUE
SP57	T1	SP57T1	8	250564	146115367	0,5	-0,022393489	1	1	TRUE
SP57	T1	SP57T1	9	117713	45372357	0,577	-0,061444841	1	0	TRUE
SP57	T1	SP57T1	9	65617649	65973595	0,565536919	-0,21442303	1	0	TRUE
SP57	T1	SP57T1	9	66455566	141069978	0,504	-0,015910647	1	1	TRUE

SP57	T10	SP57T10	10	412449	135183608	0,569	-0,2035027	1
	TRUE							
SP57	T11	SP57T11	11	193112	51459199	0,504	-0,001381129	1
	TRUE							
SP57	T11	SP57T11	11	55234785	134856661	0,5	-0,016279769	1
	TRUE							
SP57	T11	SP57T11	12	247900	133463969	0,5	-0,033454438	1
	TRUE							
SP57	T11	SP57T11	13	19059494	115064685	0,5	-0,026667167	1
	TRUE							
SP57	T11	SP57T11	14	19118067	107183367	0,502	-0,034308317	1
	TRUE							
SP57	T11	SP57T11	15	20170150	102004231	0,506	-0,026204441	1
	TRUE							
SP57	T11	SP57T11	16	240280	90162340	0,5	-0,04344366	1
	TRUE							
SP57	T11	SP57T11	17	6115	81082365	0,503	-0,041141893	1
	TRUE							
SP57	T11	SP57T11	18	348161	77895192	0,5	-0,016617552	1
	TRUE							
SP57	T11	SP57T11	19	335946	59074653	0,5	-0,069095416	1
	TRUE							
SP57	T11	SP57T11	20	138125	62899394	0,553	0,137358998	2
	TRUE							
SP57	T11	SP57T11	21	9891930	9912194	0,588618078	-0,135667838	
	0	FALSE						
SP57	T11	SP57T11	21	10793702	48083526	0,5	-0,036009183	1
	TRUE							
SP57	T11	SP57T11	22	16255826	51182485	0,563243975	-0,222017046	
	0	TRUE						
SP57	T21	SP57T21	1	900298	249212725	0,504	0,00758797	1
	TRUE							
SP57	T21	SP57T21	2	173150	233537125	0,5	0,009660613	1
	TRUE							
SP57	T21	SP57T21	2	233594875	234433081	0,657209544	-0,441043556	
	0	TRUE						
SP57	T21	SP57T21	2	234457900	242946289	0,505	-0,033531248	1
	TRUE							
SP57	T21	SP57T21	3	403690	197762623	0,5	0,00314352	1
	TRUE							
SP57	T21	SP57T21	4	60400	190904031	0,5	0,010341184	1
	TRUE							
SP57	T21	SP57T21	5	163266	180687212	0,5	0,007019969	1
	TRUE							
SP57	T21	SP57T21	6	203878	168325673	0,503	0,025987159	1
	TRUE							

SP57	T20	SP57T20TRUE	6	168347291	169617840	0,651	-0,295615239	1
SP57	T21	SP57T21TRUE	6	169619687	170892848	0,514	-0,040278044	1
SP57	T21	SP57T21TRUE	7	286534	159025494	0,6	0,30696016	2
SP57	T21	SP57T21TRUE	8	250564	146115367	0,5	-0,007217622	1
SP57	T20	SP57T20TRUE	9	117713	34500821	0,667	-0,065753874	1
SP57	T21	SP57T21TRUE	9	34723744	45372357	0,507	0,026625614	1
SP57	T20	SP57T20TRUE	9	65617649	68728799	0,677	-0,125953116	1
SP57	T21	SP57T21TRUE	9	68779054	141069978	0,5	-0,016968557	1
SP57	T21	SP57T210TRUE	10	412449	135183608	0,660871754	-0,425547565	
SP57	T21	SP57T21TRUE	11	193112	134856661	0,5	0,008367785	1
SP57	T21	SP57T21TRUE	12	247900	133463969	0,5	-0,001597439	1
SP57	T21	SP57T21TRUE	13	19059494	115064685	0,5	0,00191635	1
SP57	T21	SP57T21TRUE	14	19118067	107183367	0,5	0,00231635	1
SP57	T20	SP57T20FALSE	15	20170150	22148395	0,598	-0,008557599	1
SP57	T21	SP57T21TRUE	15	22319166	102004231	0,5	-0,045877866	1
SP57	T21	SP57T21TRUE	16	240280	90162340	0,5	-0,040583247	1
SP57	T2TRUE	SP57T2TRUE	17	6115	81082365	0,5	-0,013017528	1 1
SP57	T21	SP57T21TRUE	18	348161	77895192	0,5	0,040253986	1
SP57	T21	SP57T21TRUE	19	335946	59074653	0,504	-0,058443766	1
SP57	T21	SP57T21TRUE	20	138125	62899394	0,603	0,298682862	2
SP57	T21	SP57T21TRUE	21	9891930	48083526	0,5	-0,021341887	1
SP57	T21	SP57T21TRUE	22	16255826	16949797	0,5	-0,243916994	1
SP57	T21	SP57T210TRUE	22	16953727	51182485	0,65974096	-0,430350105	

SP57	T31	SP57T3	1	900298	249212725	0,5	0,018492201	1 TRUE
SP57	T31	SP57T3	2	173150	233536926	0,5	0,021919802	1 TRUE
SP57	T31	SP57T3	2	233537125	234433081	0,653872072	-0,35552363	0 TRUE
SP57	T31	SP57T3	2	234457900	242946289	0,507	0,024118614	1 TRUE
SP57	T31	SP57T3	3	403690	197762623	0,5	0,040271388	1 TRUE
SP57	T31	SP57T3	4	60400	190904031	0,5	0,037783326	1 TRUE
SP57	T31	SP57T3	5	163266	180687212	0,5	0,023557595	1 TRUE
SP57	T31	SP57T3	6	203878	168352105	0,506	0,033593819	1 TRUE
SP57	T31	SP57T3	6	168457966	168479790	0,657200896	-0,341581617	0 TRUE
SP57	T31	SP57T3	6	168687815	170892848	0,513	-0,031928916	1 TRUE
SP57	T31	SP57T3	7	286534	100608573	0,599	0,307136109	2 TRUE
SP57	T31	SP57T3	7	100615449	100615533	0,699056417	-0,153711331	0 FALSE
SP57	T31	SP57T3	7	100624718	159025494	0,595	0,306658119	2 TRUE
SP57	T31	SP57T3	8	250564	146115367	0,5095	0,022944625	1 TRUE
SP57	T30	SP57T3	9	117713	21440994	0,732	0,031377918	2 TRUE
SP57	T30	SP57T3	9	21816573	22748135	0,5	-0,9801894	0 TRUE
SP57	T30	SP57T3	9	23705108	34500821	0,7215	0,001574094	2 FALSE
SP57	T31	SP57T3	9	34723744	45372357	0,516	-0,015088439	1 TRUE
SP57	T31	SP57T3	9	65617649	68409631	0,671620001	-0,279584537	0 FALSE
SP57	T31	SP57T3	9	68409677	141069844	0,5	0,008540513	1 TRUE
SP57	T31	SP57T3	9	141069905	141069978	0,691045818	-0,191611181	0 TRUE
SP57	T30	SP57T3	10	412449	51540291	0,653	-0,357961798	1 TRUE
SP57	T31	SP57T3	10	51549496	51633027	0,513	-0,262357385	1 TRUE

SP57	T31	SP57T30	TRUE	10	51785598	135183608	0,647334992	-0,382516714
SP57	T31	SP57T31	TRUE	11	193112	18267135	0,506	0,060602322	1
SP57	T30	SP57T31	FALSE	11	18267353	18267478	0,698	0,179141376	2
SP57	T31	SP57T31	FALSE	11	18291063	51459199	0,513	0,023493547	1
SP57	T31	SP57T31	TRUE	11	55234785	134856661	0,5	0,025240821	1
SP57	T31	SP57T31	TRUE	12	247900	133463969	0,5	0,004387635	1
SP57	T31	SP57T31	TRUE	13	19059494	115064685	0,505	0,039346489	1
SP57	T31	SP57T31	TRUE	14	19118067	107183367	0,505	0,004386624	1
SP57	T30	SP57T31	FALSE	15	20170150	22148395	0,61	-0,073825369	1
SP57	T31	SP57T31	TRUE	15	22319166	102004231	0,5	0,011735142	1
SP57	T31	SP57T31	TRUE	16	240280	90162340	0,5	-0,034137147	1
SP57	T3TRUE	SP57T31	TRUE	17	6115	81082365	0,506	-0,016595967	1	1
SP57	T31	SP57T31	TRUE	18	348161	77895192	0,5	0,052039983	1
SP57	T31	SP57T31	TRUE	19	335946	59074653	0,5	-0,117228186	1
SP57	T31	SP57T31	TRUE	20	138125	62899394	0,5935	0,312633097	2
SP57	T30	SP57T31	TRUE	21	9891930	9912194	0,7015	-0,044468141	2
SP57	T31	SP57T31	TRUE	21	10793702	48083526	0,5	-0,020807923	1
SP57	T31	SP57T30	TRUE	22	16255826	51182485	0,6431819	-0,39940708
SP57	T41	SP57T41	TRUE	1	900298	203468792	0,5	-0,003144678	1
SP57	T41	SP57T41	FALSE	1	203652444	205042115	0,6855	0,682654935	4
SP57	T41	SP57T41	TRUE	1	205042939	249212725	0,5	-0,035004703	1
SP57	T41	SP57T41	TRUE	2	173150	233429185	0,5	-0,019096161	1
SP57	T40	SP57T41	TRUE	2	233536926	234405374	0,628	-0,380911688	1

SP57	T41	SP57T4 TRUE	2	234433081	242946289	0,506	-0,008233492	1
SP57	T41	SP57T4 TRUE	3	403690	195397908	0,5	-0,015181377	1
SP57	T40	SP57T4 0 FALSE	3	195410751	195426149	0,540223378	-0,719998123	
SP57	T41	SP57T4 TRUE	3	195475989	197762623	0,5	-0,134276355	1
SP57	T4 TRUE	SP57T4	4	60400	190904031	0,5	-0,00912679	1 1
SP57	T41	SP57T4 TRUE	5	163266	180687212	0,5	-0,020299243	1
SP57	T41	SP57T4 TRUE	6	203878	29897412	0,5	0,002265255	1
SP57	T41	SP57T4 TRUE	6	29909360	29910189	0,671	0,378538746	3
SP57	T41	SP57T4 TRUE	6	29910276	170892848	0,504	0,01205705	1
SP57	T41	SP57T4 TRUE	7	286534	100608573	0,593	0,261531289	2
SP57	T40	SP57T4 TRUE	7	100615449	100615533	0,722	0,433816035	3
SP57	T41	SP57T4 TRUE	7	100624718	159025494	0,585	0,248727317	2
SP57	T41	SP57T4 TRUE	8	250564	146115367	0,5	-0,016153796	1
SP57	T42	SP57T4 0 TRUE	9	117713	21440994	0,705663443	-0,076531749	
SP57	T40	SP57T4 TRUE	9	21816573	24545695	0,529	-0,641552208	0
SP57	T40	SP57T4 FALSE	9	24545957	34500821	0,706	-0,008279899	2
SP57	T41	SP57T4 TRUE	9	34723744	45372357	0,5	-0,00146502	1
SP57	T41	SP57T4 FALSE	9	65617649	70731810	0,645	0,066903933	2
SP57	T41	SP57T4 TRUE	9	71224796	141069978	0,5	-0,002159351	1
SP57	T40	SP57T4 TRUE	10	412449	50681033	0,638	-0,372026825	1
SP57	T41000	SP57T4 0 TRUE	10	50691009	50857835	0,998720542	-1,091421552	
SP57	T41	SP57T4 0 TRUE	10	50863147	135183608	0,638200714	-0,374254571	
SP57	T41	SP57T4 TRUE	11	193112	134856661	0,503	-0,001885627	1

SP57	T4	SP57T4	12	247900	113357442	0,505	-0,010912122	1
	1	TRUE						
SP57	T4	SP57T4	12	113376320	113376388	0,721400433	0,002741976	
	2	0 TRUE						
SP57	T4	SP57T4	12	113376452	133463969	0,5	-0,06580706	1
	1	TRUE						
SP57	T4	SP57T4	13	19059494	115064685	0,505	-0,019446308	1
	1	TRUE						
SP57	T4	SP57T4	14	19118067	107183367	0,5	-0,01417549	1
	1	TRUE						
SP57	T4	SP57T4	15	20170150	22148395	0,61	-0,114428937	1
	0	FALSE						
SP57	T4	SP57T4	15	22319166	102004231	0,505	-0,028458045	1
	1	TRUE						
SP57	T4	SP57T4	16	240280	90162340	0,5	-0,038364218	1
	1	TRUE						
SP57	T4	SP57T4	17	6115	81082365	0,5	-0,006343648	1
	1	TRUE						
SP57	T4	SP57T4	18	348161	77895192	0,5	-0,032240081	1
	1	TRUE						
SP57	T4	SP57T4	19	335946	59074653	0,5	-0,045409643	1
	1	TRUE						
SP57	T4	SP57T4	20	138125	62899394	0,5925	0,263783928	2
	1	TRUE						
SP57	T4	SP57T4	21	9891930	9912194	0,674884984	-0,2200152	
	1	0 FALSE						
SP57	T4	SP57T4	21	10793702	48083526	0,5	-0,016541719	1
	1	TRUE						
SP57	T4	SP57T4	22	16255826	28315072	0,643079815	-0,354666504	
	1	0 TRUE						
SP57	T4	SP57T4	22	28316553	28316561	0,709710257	-0,056558607	
	2	0 FALSE						
SP57	T4	SP57T4	22	28559120	51182485	0,64	-0,3606377	1
	0	TRUE						
A23	recurrent_M	A23_recurrent_M	1	13273	227381442	0,5	0,015817657	
	1	1 TRUE						
A23	recurrent_M	A23_recurrent_M	1	227681573	227681585	0,81	-	
0,286876872	1	0 FALSE						
A23	recurrent_M	A23_recurrent_M	1	227825508	248814126	0,5	-	
0,027450093	1	1 TRUE						
A23	recurrent_M	A23_recurrent_M	2	45843	243037004	0,5	-0,012336952	
	1	1 TRUE						
A23	recurrent_M	A23_recurrent_M	3	403288	197837967	0,5		
	0,003693336	1 1 TRUE						
A23	recurrent_M	A23_recurrent_M	4	195436	49554573	0,5		
	0,00250061	1 1 TRUE						

A23	recurrent_M	A23_recurrent_M	4	52714511	190903950	0,5025	0,041196172
1	1	TRUE					
A23	recurrent_M	A23_recurrent_M	5	163205	180583043	0,5	0,009974594
1	1	TRUE					
A23	recurrent_M	A23_recurrent_M	6	203722	32522419	0,5	-0,026318777
1	1	TRUE					
A23	recurrent_M	A23_recurrent_M	6	32522422	32549780	0,6275	0,106582216
2	1	TRUE					
A23	recurrent_M	A23_recurrent_M	6	32551872	170892848	0,5	-0,003700278
1	1	TRUE					
A23	recurrent_M	A23_recurrent_M	7	295970	159053596	0,506	-0,005767855
1	1	TRUE					
A23	recurrent_M	A23_recurrent_M	8	182934	146228622	0,503	0,000814989
1	1	TRUE					
A23	recurrent_M	A23_recurrent_M	9	214864	141071475	0,5	-0,016020672
1	1	TRUE					
A23	recurrent_M	A23_recurrent_M	10	132135	135381592	0,5	0,00415608
1	1	TRUE					
A23	recurrent_M	A23_recurrent_M	11	192997	134252121	0,5	0,010463417
1	1	TRUE					
A23	recurrent_M	A23_recurrent_M	12	248202	133795960	0,505	0,003976804
1	1	TRUE					
A23	recurrent_M	A23_recurrent_M	13	19059494	115030714	0,504	-0,002835674
1	1	TRUE					
A23	recurrent_M	A23_recurrent_M	14	19401146	107178965	0,5	-0,014568802
1	1	TRUE					
A23	recurrent_M	A23_recurrent_M	15	20173245	102304498	0,5	-0,00063043
1	1	TRUE					
A23	recurrent_M	A23_recurrent_M	16	97610	90133064	0,5	-0,047433987
1	1	TRUE					
A23	recurrent_M	A23_recurrent_M	17	6177	81006629	0,5	-0,035057231
1	1	TRUE					
A23	recurrent_M	A23_recurrent_M	18	204780	77926862	0,507	0,004150848
1	1	TRUE					
A23	recurrent_M	A23_recurrent_M	19	312164	59082605	0,5	-0,061304882
1	1	TRUE					
A23	recurrent_M	A23_recurrent_M	20	76962	62903550	0,5	-0,003266219
1	1	TRUE					
A23	recurrent_M	A23_recurrent_M	21	9891930	48078611	0,5	-0,038168269
1	1	TRUE					
A23	recurrent_M	A23_recurrent_M	22	16393311	51219006	0,504	-0,017582104
1	1	TRUE					
A23	recurrent_S	A23_recurrent_S	1	13273	248814126	0,504	0,028071474
1	1	TRUE					
A23	recurrent_S	A23_recurrent_S	2	45843	243037004	0,5	0,024081542
1	1	TRUE					

A23	recurrent_S	A23_recurrent_S	3	403288	180490822	0,5	0,020451259
1	1	TRUE					
A23	recurrent_S	A23_recurrent_S	3	180703663	183904232	0,694	0,662357692
2	1	TRUE					
A23	recurrent_S	A23_recurrent_S	3	183952773	197837967	0,505	-0,00058108
1	1	TRUE					
A23	recurrent_S	A23_recurrent_S	4	195436	190903950	0,5	0,048661668
1	1	TRUE					
A23	recurrent_S	A23_recurrent_S	5	163205	180583043	0,5	0,031512563
1	1	TRUE					
A23	recurrent_S	A23_recurrent_S	6	203722	32522413	0,5	-0,008346488
1	1	TRUE					
A23	recurrent_S	A23_recurrent_S	6	32522416	32548544	0,6605	0,297740424
2	1	TRUE					
A23	recurrent_S	A23_recurrent_S	6	32548581	170892848	0,5	0,032981654
1	1	TRUE					
A23	recurrent_S	A23_recurrent_S	7	295970	53930969	0,5	0,025182383
1	1	TRUE					
A23	recurrent_S	A23_recurrent_S	7	54826830	55249063	0,772	1,033052541
3	1	TRUE					
A23	recurrent_S	A23_recurrent_S	7	55433880	159053596	0,5	0,016656327
1	1	TRUE					
A23	recurrent_S	A23_recurrent_S	8	182934	146228622	0,5	0,02062829
1	1	TRUE					
A23	recurrent_S	A23_recurrent_S	9	214864	65973564	0,5	-0,014402553
1	1	TRUE					
A23	recurrent_S	A23_recurrent_S	9	66059082	66455647	0,745	-0,035909052
1	0	FALSE					
A23	recurrent_S	A23_recurrent_S	9	66457475	141071475	0,5	-0,035642067
1	1	TRUE					
A23	recurrent_S	A23_recurrent_S	10	132135	135381592	0,5	-0,001131914
1	1	TRUE					
A23	recurrent_S	A23_recurrent_S	11	192997	134252121	0,5	0,004030965
1	1	TRUE					
A23	recurrent_S	A23_recurrent_S	12	248202	133795960	0,5	0,007031411
1	1	TRUE					
A23	recurrent_S	A23_recurrent_S	13	19059494	115030714	0,5	0,022916495
1	1	TRUE					
A23	recurrent_S	A23_recurrent_S	14	19401146	107178965	0,5	0,003918778
1	1	TRUE					
A23	recurrent_S	A23_recurrent_S	15	20173245	102304498	0,5	-0,000712915
1	1	TRUE					
A23	recurrent_S	A23_recurrent_S	16	97610	90133064	0,5	-0,040852975
1	1	TRUE					
A23	recurrent_S	A23_recurrent_S	17	6177	81006629	0,5	-0,022955149
1	1	TRUE					

A23	recurrent_S	A23_recurrent_S	18	204780	77926862	0,507	0,009332901
1	1	TRUE					
A23	recurrent_S	A23_recurrent_S	19	312164	59082605	0,5	-0,058843755
1	1	TRUE					
A23	recurrent_S	A23_recurrent_S	20	76962	62903550	0,5	-0,002134446
1	1	TRUE					
A23	recurrent_S	A23_recurrent_S	21	9891930	48078611	0,5	0,001127176
1	1	TRUE					
A23	recurrent_S	A23_recurrent_S	22	16393311	51219006	0,5	-0,017431828
1	1	TRUE					
A23	recurrent_T	A23_recurrent_T	1	13273	72740634	0,5	-0,017969459
2	2	TRUE					
A23	recurrent_T	A23_recurrent_T	1	74664149	99753631	0,639	-0,293158688
2	0	TRUE					
A23	recurrent_T	A23_recurrent_T	1	100715454	227381442	0,507	0,072834435
2	2	TRUE					
A23	recurrent_T	A23_recurrent_T	1	227681573	227681585	0,591772815	-0,500010316
1	0	FALSE					
A23	recurrent_T	A23_recurrent_T	1	227825508	248814126	0,5	0,012873827
2	2	TRUE					
A23	recurrent_T	A23_recurrent_T	2	45843	91885946	0,604	0,006274487
3	1	TRUE					
A23	recurrent_T	A23_recurrent_T	2	95824624	243037004	0,509	0,182538454
3	3	TRUE					
A23	recurrent_T	A23_recurrent_T	3	403288	180703663	0,5	0,034415589
2	2	TRUE					
A23	recurrent_T	A23_recurrent_T	3	182681740	183056541	0,94	3,204043997
75	2	TRUE					
A23	recurrent_T	A23_recurrent_T	3	183904232	197837967	0,5	-0,015727512
2	2	TRUE					
A23	recurrent_T	A23_recurrent_T	4	195436	190903950	0,5	0,067095517
2	2	TRUE					
A23	recurrent_T	A23_recurrent_T	5	163205	180583043	0,503	0,05111449
2	2	TRUE					
A23	recurrent_T	A23_recurrent_T	6	203722	32522419	0,5	0,002210913
2	2	TRUE					
A23	recurrent_T	A23_recurrent_T	6	32522422	32522425	0,805111503	0,566713006
8	0	TRUE					
A23	recurrent_T	A23_recurrent_T	6	32522427	33047432	0,5	0,044682619
2	2	TRUE					
A23	recurrent_T	A23_recurrent_T	6	33048380	33053812	0,632	0,09587161
4	1	TRUE					
A23	recurrent_T	A23_recurrent_T	6	33060064	57841320	0,503	0,047755816
2	2	TRUE					
A23	recurrent_T	A23_recurrent_T	6	58776965	58778809	0,5	-3,20144033
0	0	TRUE					

A23	recurrent_T	A23_recurrent_T	6	62407067	170892848	0,5	0,073483566
2	2	TRUE					
A23	recurrent_T	A23_recurrent_T	7	295970	13911420	0,506	0,081365175
2	2	TRUE					
A23	recurrent_T	A23_recurrent_T	7	13946316	32529936	0,591	0,34285473
4	2	TRUE					
A23	recurrent_T	A23_recurrent_T	7	32535437	43686224	0,644	0,252167444
4	1	TRUE					
A23	recurrent_T	A23_recurrent_T	7	43687296	53930969	0,606	0,301724199
4	2	FALSE					
A23	recurrent_T	A23_recurrent_T	7	54826830	55249063	0,963	3,773147354
116	2	TRUE					
A23	recurrent_T	A23_recurrent_T	7	55433880	128312463	0,563	0,144190995
3	2	FALSE					
A23	recurrent_T	A23_recurrent_T	7	128315882	159053596	0,591	0,359314279
4	2	TRUE					
A23	recurrent_T	A23_recurrent_T	8	182934	146228622	0,504	0,056607865
2	2	TRUE					
A23	recurrent_T	A23_recurrent_T	9	214864	90342675	0,5	0,001987417
2	2	TRUE					
A23	recurrent_T	A23_recurrent_T	9	90343780	141071475	0,514	-0,154529243
1	1	FALSE					
A23	recurrent_T	A23_recurrent_T	10	132135	38737254	0,633	-0,348591374
2	0	TRUE					
A23	recurrent_T	A23_recurrent_T	10	43315692	62548098	0,516	-0,078390706
2	2	FALSE					
A23	recurrent_T	A23_recurrent_T	10	62634621	135381592	0,64	-0,310602217
2	0	TRUE					
A23	recurrent_T	A23_recurrent_T	11	192997	134252121	0,554	-0,116912788
2	1	TRUE					
A23	recurrent_T	A23_recurrent_T	12	248202	133795960	0,5	0,00075688
2	2	TRUE					
A23	recurrent_T	A23_recurrent_T	13	19059494	115030714	0,5	-0,124906757
2	2	TRUE					
A23	recurrent_T	A23_recurrent_T	14	19401146	107178965	0,5	0,02699028
2	2	TRUE					
A23	recurrent_T	A23_recurrent_T	15	20173245	20462603	0,503	-0,387124124
1	1	TRUE					
A23	recurrent_T	A23_recurrent_T	15	20466604	20489310	0,695153577	-0,078720673
3	0	TRUE					
A23	recurrent_T	A23_recurrent_T	15	20643927	102304498	0,5	0,019756485
2	2	TRUE					
A23	recurrent_T	A23_recurrent_T	16	97610	33613219	0,565	-0,252062216
2	1	TRUE					
A23	recurrent_T	A23_recurrent_T	16	33740747	46405156	0,5	-2,502044132
0	0	TRUE					

A23	recurrent_T	A23_recurrent_T	16	46407745	90133064	0,562	-0,209498362	2	1	TRUE
A23	recurrent_T	A23_recurrent_T	17	6177	81006629	0,5	-0,050998416	2	2	TRUE
A23	recurrent_T	A23_recurrent_T	18	204780	77926862	0,505	0,038154148	2	2	TRUE
A23	recurrent_T	A23_recurrent_T	19	312164	59082605	0,5	-0,139500774	1	1	TRUE
A23	recurrent_T	A23_recurrent_T	20	76962	62903550	0,5	0,016809432	2	2	TRUE
A23	recurrent_T	A23_recurrent_T	21	9891930	48078611	0,5	0,005594123	2	2	TRUE
A23	recurrent_T	A23_recurrent_T	22	16393311	51219006	0,55	-0,158524191	2	1	FALSE
A34	S1	A34S1	1	907609	203317204	0,506	-0,044749403	1	1	TRUE
A34	S1	A34S1	1	203766827	204516025	0,849	2,03229278	7	1	FALSE
A34	S1	A34S1	1	204915347	249107414	0,5	-0,02311113	1	1	TRUE
A34	S1	A34S1	2	224970	242842568	0,5	-0,010526313	1	1	TRUE
A34	S1	A34S1	3	361508	89528477	0,505	0,030055522	1	1	TRUE
A34	S1	A34S1	3	93593119	197402254	0,502	-0,064848986	1	1	TRUE
A34	S1	A34S1	4	60400	49063872	0,5	-0,041947205	1	1	TRUE
A34	S1	A34S1	4	52714511	55593464	0,6935	0,580580441	2	1	TRUE
A34	S1	A34S1	4	55946171	190395259	0,5	0,015031789	1	1	TRUE
A34	S1	A34S1	5	163205	180665998	0,5	0,064808993	1	1	TRUE
A34	S1	A34S1	6	335251	170887693	0,5	-0,059453122	1	1	TRUE
A34	S1	A34S1	7	296739	54621692	0,562	0,12644481	1	1	FALSE
A34	S1	A34S1	7	55214348	55229255	0,8585	1,655938289	6	1	TRUE
A34	S1	A34S1	7	55780176	76126737	0,582	-0,092330174	1	1	FALSE
A34	S1	A34S1	7	76131645	76751357	0,7735	-1,402691865	0	0	TRUE
A34	S1	A34S1	7	76751543	158827326	0,574	0,187482596	1	1	FALSE

A34	S1	A34S1	8	196274	146228622	0,501	-0,037442141	1	1	TRUE
A34	S1	A34S1	9	154795	141016262	0,5	-0,067944124	1	1	TRUE
A34	S1	A34S1	10	1018585	135381276	0,5	-0,137075568	1	1	TRUE
A34	S1	A34S1	11	193865	134856661	0,506	0,028875112	1	1	TRUE
A34	S1	A34S1	12	250239	133796033	0,504	-0,02840592	1	1	TRUE
A34	S1	A34S1	13	19600475	115064542	0,5	-0,008844078	1	1	TRUE
A34	S1	A34S1	14	19889910	107178965	0,5	0,043843364	1	1	TRUE
A34	S1	A34S1	15	20446043	102312835	0,505	-0,015042837	1	1	TRUE
A34	S1	A34S1	16	129531	90161231	0,5	-0,084941141	1	1	TRUE
A34	S1	A34S1	17	171098	81050982	0,5055	-0,000514558	1	1	TRUE
A34	S1	A34S1	18	203081	77805856	0,507	0,002138314	1	1	TRUE
A34	S1	A34S1	19	288062	59022697	0,5	-0,075676323	1	1	TRUE
A34	S1	A34S1	20	138125	35467713	0,5	-0,010455848	1	1	TRUE
A34	S1	A34S1	20	35559352	36612084	0,871	2,129919273	7	1	TRUE
A34	S1	A34S1	20	36841756	62903550	0,5	-0,093247153	1	1	TRUE
A34	S1	A34S1	21	10793925	47976203	0,505	-0,030724512	1	1	TRUE
A34	S1	A34S1	22	17054291	51207180	0,5	-0,049397962	1	1	TRUE
A34	S2	A34S2	1	907609	203317204	0,5	-0,042663364	1	1	TRUE
A34	S2	A34S2	1	203766827	204516025	0,8655	2,090597554	7	1	TRUE
A34	S2	A34S2	1	204915347	249107414	0,502	0,037048765	1	1	TRUE
A34	S2	A34S2	2	224970	242842568	0,5	0,016168494	1	1	TRUE
A34	S2	A34S2	3	361508	197402254	0,5	0,010728641	1	1	TRUE
A34	S2	A34S2	4	60400	49063872	0,5	-0,046944479	1	1	TRUE

A34	S2	A34S2	4	52714511	55593464	0,75	0,869460936	3	1
	TRUE								
A34	S2	A34S2	4	55946171	190395259	0,5	0,077512822	1	1
	TRUE								
A34	S2	A34S2	5	163205	180665998	0,5	0,086177031	1	1
	TRUE								
A34	S2	A34S2	6	335251	31085269	0,5	-0,097172772	1	1
	TRUE								
A34	S2	A34S2	6	31088145	31088241	0,737	-0,844456054	1	1
	TRUE								
A34	S2	A34S2	6	31097453	57467175	0,503	-0,042077484	1	1
	TRUE								
A34	S2	A34S2	6	62442604	170887693	0,5	-0,002786999	1	1
	TRUE								
A34	S2	A34S2	7	296739	5105133	0,58	0,176856776	1	1
	FALSE								
A34	S2	A34S2	7	5112108	5338770	0,735	-0,007827874	1	0
	FALSE								
A34	S2	A34S2	7	5340002	54621692	0,57	0,190067276	1	1
	FALSE								
A34	S2	A34S2	7	55214348	55229255	0,9025	2,109533485	8	1
	TRUE								
A34	S2	A34S2	7	55780176	158827326	0,583	0,184725228	1	1
	FALSE								
A34	S2	A34S2	8	196274	146228622	0,5	-0,021780123	1	1
	TRUE								
A34	S2	A34S2	9	154795	141016262	0,5	-0,054133932	1	1
	TRUE								
A34	S2	A34S2	10	1018585	38645403	0,507	-0,067815226	1	1
	TRUE								
A34	S2	A34S2	10	42907201	135381276	0,563	-0,160907285	1	1
	FALSE								
A34	S2	A34S2	11	193865	134856661	0,504	0,021082155	1	1
	TRUE								
A34	S2	A34S2	12	250239	133796033	0,502	-0,009296027	1	1
	TRUE								
A34	S2	A34S2	13	19600475	115064542	0,506	0,048269973	1	1
	TRUE								
A34	S2	A34S2	14	19889910	107178965	0,503	0,048688651	1	1
	TRUE								
A34	S2	A34S2	15	20446043	102312835	0,506	0,002038367	1	1
	TRUE								
A34	S2	A34S2	16	129531	90161231	0,5	-0,104117485	1	1
	TRUE								
A34	S2	A34S2	17	171098	81050982	0,5	-0,011157076	1	1
	TRUE								

A34	S2	A34S2	18	203081	77805856	0,5055	0,063257924	1	1	TRUE
A34	S2	A34S2	19	288062	59022697	0,5	-0,117514349	1	1	TRUE
A34	S2	A34S2	20	138125	35467713	0,5	-0,012114044	1	1	TRUE
A34	S2	A34S2	20	35559352	36612084	0,8645	2,154980006	7	1	TRUE
A34	S2	A34S2	20	36841756	62903550	0,5	-0,064094196	1	1	TRUE
A34	S2	A34S2	21	10793925	47976203	0,506	-0,021019978	1	1	TRUE
A34	S2	A34S2	22	17054291	51207180	0,5	-0,058839791	1	1	TRUE
A34	S3	A34S3	1	907609	1585642	0,504	-0,356991371	1	1	TRUE
A34	S3	A34S3	1	1633004	1635193	0,528	-2,803441637	0	0	TRUE
A34	S3	A34S3	1	1635565	249107414	0,504	-0,027626182	1	1	TRUE
A34	S3	A34S3	2	224970	242842568	0,5	-0,021507729	1	1	TRUE
A34	S3	A34S3	3	361508	197402254	0,5	-0,019421131	1	1	TRUE
A34	S3	A34S3	4	60400	190395259	0,5	-0,006617131	1	1	TRUE
A34	S3	A34S3	5	163205	180665998	0,5015	0,055865451	1	1	TRUE
A34	S3	A34S3	6	335251	29797639	0,503	0,026943666	1	1	TRUE
A34	S3	A34S3	6	29910402	29911228	0,654	-1,84595394	0	0	TRUE
A34	S3	A34S3	6	29912098	170887693	0,5	-0,036994621	1	1	TRUE
A34	S3	A34S3	7	296739	5172223	0,5	-0,038622126	1	1	TRUE
A34	S3	A34S3	7	5338714	5352659	0,781	-0,670334137	1	0	TRUE
A34	S3	A34S3	7	5369522	158827326	0,5	-0,069987741	1	1	TRUE
A34	S3	A34S3	8	196274	146228622	0,503	-0,034370078	1	1	TRUE
A34	S3	A34S3	9	154795	141016262	0,503	-0,048786497	1	1	TRUE
A34	S3	A34S3	10	1018585	26505822	0,503	0,057547867	1	1	TRUE

A34	S3	A34S3	10	26991037	26993725	0,6	-0,196707569	1	1
	TRUE								
A34	S3	A34S3	10	26993728	135381276	0,503	-0,025434253	1	1
	TRUE								
A34	S3	A34S3	11	193865	134856661	0,504	0,028698691	1	1
	TRUE								
A34	S3	A34S3	12	250239	133796033	0,503	-0,02359901	1	1
	TRUE								
A34	S3	A34S3	13	19600475	115064542	0,507	0,02516228	1	1
	TRUE								
A34	S3	A34S3	14	19889910	20444012	0,539	-0,410506845	1	1
	TRUE								
A34	S3	A34S3	14	20444026	107178965	0,504	0,047060495	1	1
	TRUE								
A34	S3	A34S3	15	20446043	102312835	0,503	0,033902907	1	1
	TRUE								
A34	S3	A34S3	16	129531	1275309	0,507	-0,236932233	1	1
	TRUE								
A34	S3	A34S3	16	1279537	1279574	0,867	-1,544722906	1	0
	TRUE								
A34	S3	A34S3	16	1306346	90161231	0,5	-0,055995325	1	1
	TRUE								
A34	S3	A34S3	17	171098	81050982	0,5	0,009557557	1	1
	TRUE								
A34	S3	A34S3	18	203081	77805856	0,5	0,026573005	1	1
	TRUE								
A34	S3	A34S3	19	288062	59022697	0,5	-0,050372785	1	1
	TRUE								
A34	S3	A34S3	20	138125	62903550	0,5	-0,027625919	1	1
	TRUE								
A34	S3	A34S3	21	10793925	47976203	0,505	-0,012903281	1	1
	TRUE								
A34	S3	A34S3	22	17054291	51207180	0,5	-0,039557645	1	1
	TRUE								
A34	T1	A34T1	1	907609	1585597	0,5	-0,328372716	1	1
	TRUE								
A34	T1	A34T1	1	1585642	1633007	0,541	-2,761429416	0	0
	TRUE								
A34	T1	A34T1	1	1635193	203317204	0,5	-0,038078634	1	1
	TRUE								
A34	T1	A34T1	1	203766827	204516025	0,9495	3,430598913	20	1
	TRUE								
A34	T1	A34T1	1	204915347	249107414	0,5	-0,008998457	1	1
	TRUE								
A34	T1	A34T1	2	224970	70162534	0,5	0,027423382	1	1
	TRUE								

A34	T1	A34T1	2	70677994	91809385	0,711	-0,310441624	1	0 FALSE
A34	T1	A34T1	2	95537330	242842568	0,5	0,010638113	1	1 TRUE
A34	T1	A34T1	3	361508	197402254	0,5	0,001968955	1	1 TRUE
A34	T1	A34T1	4	60400	49063872	0,5	-0,04883049	1	1 TRUE
A34	T1	A34T1	4	52714511	55593464	0,7965	1,456232391	4	1 TRUE
A34	T1	A34T1	4	55946171	190395259	0,507	0,040849067	1	1 TRUE
A34	T1	A34T1	5	163205	180665998	0,5	0,069185644	1	1 TRUE
A34	T1	A34T1	6	335251	170887693	0,5	-0,030277924	1	1 TRUE
A34	T1	A34T1	7	296739	11419378	0,67	0,411969481	2	1 TRUE
A34	T1	A34T1	7	11464297	27566053	0,612	0,342410331	2	1 FALSE
A34	T1	A34T1	7	28449965	54621692	0,667	0,573432761	2	1 TRUE
A34	T1	A34T1	7	55214348	55229255	0,9735	3,932644216	30	1 TRUE
A34	T1	A34T1	7	55780176	158827326	0,668	0,519478861	2	1 TRUE
A34	T1	A34T1	8	196274	146228622	0,503	-0,029395479	1	1 TRUE
A34	T1	A34T1	9	154795	27455095	0,6815	-0,521525357	1	0 FALSE
A34	T1	A34T1	9	27556780	37974743	0,587	-0,268302557	1	1 FALSE
A34	T1	A34T1	9	66499220	141016262	0,5	-0,038093198	1	1 TRUE
A34	T1	A34T1	10	1018585	25888180	0,6915	-0,400763199	1	0 FALSE
A34	T1	A34T1	10	26241025	33552695	0,504	0,035668245	1	1 TRUE
A34	T1	A34T1	10	35320355	38645403	0,68	-0,513921783	1	0 FALSE
A34	T1	A34T1	10	42907201	47000146	0,53	-0,431212497	1	1 TRUE
A34	T1	A34T1	10	47667380	135381276	0,696	-0,487081401	1	0 FALSE
A34	T1	A34T1	11	193865	134856661	0,505	0,030087418	1	1 TRUE

A34	T1	A34T1	12	250239	133796033	0,5	-0,004838114	1	1
	TRUE								
A34	T1	A34T1	13	19600475	115064542	0,505	0,034944016	1	1
	TRUE								
A34	T1	A34T1	14	19889910	20444012	0,517	0,013747426	1	1
	TRUE								
A34	T1	A34T1	14	20444026	107178965	0,502	0,062151497	1	1
	TRUE								
A34	T1	A34T1	15	20446043	30008977	0,5	0,005039539	1	1
	TRUE								
A34	T1	A34T1	15	30018553	60644074	0,585	-0,177183637	1	1
	FALSE								
A34	T1	A34T1	15	60685176	102312835	0,505	0,050298729	1	1
	TRUE								
A34	T1	A34T1	16	129531	90161231	0,5	-0,088883184	1	1
	TRUE								
A34	T1	A34T1	17	171098	81050982	0,5	-0,009525389	1	1
	TRUE								
A34	T1	A34T1	18	203081	77805856	0,5	0,041242142	1	1
	TRUE								
A34	T1	A34T1	19	288062	48255804	0,5	-0,085952753	1	1
	TRUE								
A34	T1	A34T1	19	48258551	48258578	0,895	-0,867801806	1	0
	TRUE								
A34	T1	A34T1	19	48259220	59022697	0,502	-0,067260015	1	1
	TRUE								
A34	T1	A34T1	20	138125	35467713	0,5	-0,012503563	1	1
	TRUE								
A34	T1	A34T1	20	35559352	36612084	0,9525	3,504189102	21	1
	TRUE								
A34	T1	A34T1	20	36841756	62903550	0,5	-0,078243818	1	1
	TRUE								
A34	T1	A34T1	21	10793925	47976203	0,506	-0,035668281	1	1
	TRUE								
A34	T1	A34T1	22	17054291	51207180	0,5	-0,058911667	1	1
	TRUE								
A34	T2	A34T2	1	907609	203317204	0,5	-0,042476072	1	1
	TRUE								
A34	T2	A34T2	1	203766827	204516025	0,8275	1,705918345	5	1
	TRUE								
A34	T2	A34T2	1	204915347	249107414	0,5	-0,002389783	1	1
	TRUE								
A34	T2	A34T2	2	224970	242842568	0,5	-0,048048464	1	1
	TRUE								
A34	T2	A34T2	3	361508	73024350	0,505	0,045386348	1	1
	TRUE								

A34	T2	A34T2	3	73046544	73110076	0,85	-0,496762815	1	0
TRUE									
A34	T2	A34T2	3	73111368	197402254	0,5	-0,07742144	1	1
TRUE									
A34	T2	A34T2	4	60400	190395259	0,5	-0,030802273	1	1
TRUE									
A34	T2	A34T2	5	163205	180665998	0,502	0,058104619	1	1
TRUE									
A34	T2	A34T2	6	335251	170887693	0,5	-0,049195017	1	1
TRUE									
A34	T2	A34T2	7	296739	54621692	0,5	0,023998171	1	1
TRUE									
A34	T2	A34T2	7	55214348	55229255	0,857	1,580810895	6	1
TRUE									
A34	T2	A34T2	7	55780176	158827326	0,533	0,044016043	1	1
FALSE									
A34	T2	A34T2	8	196274	146228622	0,5	-0,040401651	1	1
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A34	T2	A34T2	9	154795	141016262	0,5	-0,063858741	1	1
TRUE									
A34	T2	A34T2	10	1018585	135381276	0,505	-0,082258376	1	1
TRUE									
A34	T2	A34T2	11	193865	134856661	0,504	0,026489135	1	1
TRUE									
A34	T2	A34T2	12	250239	133796033	0,502	-0,018545614	1	1
TRUE									
A34	T2	A34T2	13	19600475	115064542	0,504	-0,006885215	1	1
TRUE									
A34	T2	A34T2	14	19889910	107178965	0,5	0,04966529	1	1
TRUE									
A34	T2	A34T2	15	20446043	102312835	0,505	-0,001743645	1	1
TRUE									
A34	T2	A34T2	16	129531	90161231	0,503	-0,080808631	1	1
TRUE									
A34	T2	A34T2	17	171098	81050982	0,5	-0,005269794	1	1
TRUE									
A34	T2	A34T2	18	203081	77805856	0,5	0,01552285	1	1
TRUE									
A34	T2	A34T2	19	288062	59022697	0,5	-0,085996046	1	1
TRUE									
A34	T2	A34T2	20	138125	35467713	0,5	-0,000892178	1	1
TRUE									
A34	T2	A34T2	20	35559352	36612084	0,82	1,676473718	5	1
TRUE									
A34	T2	A34T2	20	36841756	62903550	0,5	-0,068830669	1	1
TRUE									

A34	T2	A34T2	21	10793925	47976203	0,5	-0,037593742	1	1	TRUE
A34	T2	A34T2	22	17054291	51207180	0,5	-0,041365274	1	1	TRUE
A34	T3	A34T3	1	907609	1585642	0,519	-0,180687268	1	1	TRUE
A34	T3	A34T3	1	1633004	1635193	0,55	-2,498407509	0	0	TRUE
A34	T3	A34T3	1	1635565	120539331	0,5	-0,014285646	1	1	TRUE
A34	T3	A34T3	1	120572547	120611964	0,684	-1,264137196	0	0	TRUE
A34	T3	A34T3	1	144854597	203317204	0,502	-0,048360486	1	1	TRUE
A34	T3	A34T3	1	203766827	204516025	0,8895	2,197903713	8	1	TRUE
A34	T3	A34T3	1	204915347	249107414	0,5	-0,060356911	1	1	TRUE
A34	T3	A34T3	2	224970	242842568	0,5	-0,108077146	1	1	TRUE
A34	T3	A34T3	3	361508	197402254	0,505	-0,057013455	1	1	TRUE
A34	T3	A34T3	4	60400	190395259	0,5	-0,115451939	1	1	TRUE
A34	T3	A34T3	5	163205	180665998	0,5	-0,007750512	1	1	TRUE
A34	T3	A34T3	6	335251	170887693	0,5	-0,083565916	1	1	TRUE
A34	T3	A34T3	7	296739	5105133	0,5885	0,363451926	1	1	FALSE
A34	T3	A34T3	7	5112108	5340002	0,667	-0,724175424	1	1	TRUE
A34	T3	A34T3	7	5347914	54621692	0,569	0,104236813	1	1	FALSE
A34	T3	A34T3	7	55214348	55229255	0,888	2,175368057	8	1	TRUE
A34	T3	A34T3	7	55780176	158827326	0,587	0,158173365	1	1	FALSE
A34	T3	A34T3	8	196274	146228622	0,503	-0,095677534	1	1	TRUE
A34	T3	A34T3	9	154795	141016262	0,5	-0,055515651	1	1	TRUE
A34	T3	A34T3	10	1018585	38645403	0,507	-0,163708533	1	1	TRUE
A34	T3	A34T3	10	42907201	135381276	0,536	-0,215894263	1	1	FALSE

A34	T3	A34T3	11	193865	134856661	0,503	0,037851689	1	1
TRUE									
A34	T3	A34T3	12	250239	133796033	0,503	-0,075470985	1	1
TRUE									
A34	T3	A34T3	13	19600475	115064542	0,504	-0,100716336	1	1
TRUE									
A34	T3	A34T3	14	19889910	107178965	0,5	0,016562565	1	1
TRUE									
A34	T3	A34T3	15	20446043	60689995	0,525	-0,163743185	1	1
FALSE									
A34	T3	A34T3	15	60690089	102312835	0,505	0,039060526	1	1
TRUE									
A34	T3	A34T3	16	129531	1275309	0,504	-0,055067239	1	1
TRUE									
A34	T3	A34T3	16	1279537	1279574	0,875	-1,332730303	1	0
TRUE									
A34	T3	A34T3	16	1306346	90161231	0,5	-0,010891581	1	1
TRUE									
A34	T3	A34T3	17	171098	81050982	0,5	0,046428128	1	1
TRUE									
A34	T3	A34T3	18	203081	77805856	0,5	-0,098354396	1	1
TRUE									
A34	T3	A34T3	19	288062	59022697	0,5	-0,058183435	1	1
TRUE									
A34	T3	A34T3	20	138125	35467713	0,5	0,026676543	1	1
TRUE									
A34	T3	A34T3	20	35559352	36612084	0,8885	2,307402189	9	1
FALSE									
A34	T3	A34T3	20	36841756	62903550	0,5	0,00303765	1	1
TRUE									
A34	T3	A34T3	21	10793925	47976203	0,505	0,009838616	1	1
TRUE									
A34	T3	A34T3	22	17054291	51207180	0,5	0,046160442	1	1
TRUE									
A34	T4	A34T4	1	907609	120539331	0,5	-0,049077582	1	1
TRUE									
A34	T4	A34T4	1	120572547	120611964	0,687	-1,238608882	0	0
TRUE									
A34	T4	A34T4	1	144854597	203317204	0,5	-0,036942527	1	1
TRUE									
A34	T4	A34T4	1	203766827	204516025	0,934	3,121688703	16	1
TRUE									
A34	T4	A34T4	1	204915347	249107414	0,5	-0,023802196	1	1
TRUE									
A34	T4	A34T4	2	224970	70162534	0,503	-0,02149379	1	1
TRUE									

A34	T4	A34T4	2	70677994	91809385	0,65	-0,222863899	1	1 FALSE
A34	T4	A34T4	2	95537330	242842568	0,5	-0,016232227	1	1 TRUE
A34	T4	A34T4	3	361508	89528477	0,505	0,02719889	1	1 TRUE
A34	T4	A34T4	3	93593119	197402254	0,502	-0,088217393	1	1 TRUE
A34	T4	A34T4	4	60400	49063872	0,504	-0,068384608	1	1 TRUE
A34	T4	A34T4	4	52714511	55593464	0,8155	1,285701415	4	1 TRUE
A34	T4	A34T4	4	55946171	190395259	0,5045	-0,011425336	1	1 TRUE
A34	T4	A34T4	5	163205	180665998	0,5	0,055585219	1	1 TRUE
A34	T4	A34T4	6	335251	170887693	0,5	-0,060872343	1	1 TRUE
A34	T4	A34T4	7	296739	7613039	0,649	0,39110486	2	1 FALSE
A34	T4	A34T4	7	10973362	27239193	0,591	0,20926734	1	1 FALSE
A34	T4	A34T4	7	27497389	54621692	0,645	0,427226388	2	1 FALSE
A34	T4	A34T4	7	55214348	55229255	0,957	3,1760052	18	1 TRUE
A34	T4	A34T4	7	55780176	158827326	0,644	0,384716496	2	1 FALSE
A34	T4	A34T4	8	196274	146228622	0,5	-0,047011777	1	1 TRUE
A34	T4	A34T4	9	154795	27290984	0,639	-0,439078765	1	1 FALSE
A34	T4	A34T4	9	27296705	141016262	0,503	-0,057229106	1	1 TRUE
A34	T4	A34T4	10	1018585	26505822	0,6405	-0,326443532	1	1 FALSE
A34	T4	A34T4	10	26991037	26993725	0,639	0,126318713	2	1 TRUE
A34	T4	A34T4	10	26993728	47000146	0,529	-0,284324505	1	1 FALSE
A34	T4	A34T4	10	47667380	135381276	0,646	-0,417821307	1	1 FALSE
A34	T4	A34T4	11	193865	134856661	0,502	0,006853732	1	1 TRUE
A34	T4	A34T4	12	250239	133796033	0,5	-0,053329958	1	1 TRUE

A34	T4	A34T4	13	19600475	115064542	0,505	-0,004239228	1	1	TRUE
A34	T4	A34T4	14	19889910	107178965	0,5	0,03582738	1	1	TRUE
A34	T4	A34T4	15	20446043	31793930	0,507	-0,059607169	1	1	TRUE
A34	T4	A34T4	15	32620127	59972372	0,6	-0,269882588	1	1	FALSE
A34	T4	A34T4	15	59981515	102312835	0,5	0,037252699	1	1	TRUE
A34	T4	A34T4	16	129531	90161231	0,504	-0,072014866	1	1	TRUE
A34	T4	A34T4	17	171098	81050982	0,5	0,014475977	1	1	TRUE
A34	T4	A34T4	18	203081	77805856	0,5	0,008024797	1	1	TRUE
A34	T4	A34T4	19	288062	59022697	0,5	-0,050902806	1	1	TRUE
A34	T4	A34T4	20	138125	35467713	0,5	-0,044977978	1	1	TRUE
A34	T4	A34T4	20	35559352	36612084	0,9315	3,188010265	17	1	FALSE
A34	T4	A34T4	20	36841756	62903550	0,504	-0,051053515	1	1	TRUE
A34	T4	A34T4	21	10793925	47976203	0,5	-0,026207014	1	1	TRUE
A34	T4	A34T4	22	17054291	51207180	0,5	-0,031528966	1	1	TRUE
A34	T5	A34T5	1	907609	203317204	0,5	-0,028212121	1	1	TRUE
A34	T5	A34T5	1	203766827	204516025	0,9605	3,872177922	28	1	TRUE
A34	T5	A34T5	1	204915347	249107414	0,502	0,03622707	1	1	TRUE
A34	T5	A34T5	2	224970	70162534	0,5	0,053026891	1	1	TRUE
A34	T5	A34T5	2	70677994	91809385	0,777	-0,376089162	1	0	FALSE
A34	T5	A34T5	2	95537330	242842568	0,5	0,06669349	1	1	TRUE
A34	T5	A34T5	3	361508	197402254	0,5	0,017103982	1	1	TRUE
A34	T5	A34T5	4	60400	49063872	0,5	-0,027591541	1	1	TRUE
A34	T5	A34T5	4	52714511	55593464	0,873	1,894811146	7	1	TRUE

A34	T5	A34T5	4	55946171	190395259	0,5	0,053102814	1	1
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A34	T5	A34T5	5	163205	180665998	0,5	0,090087264	1	1
TRUE									
A34	T5	A34T5	6	335251	170887693	0,5	-0,036521773	1	1
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A34	T5	A34T5	7	296739	54621692	0,667	0,539877029	2	1
TRUE									
A34	T5	A34T5	7	55214348	55229255	0,9835	4,582564246	47	1
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A34	T5	A34T5	7	55780176	158827326	0,685	0,600866043	2	1
FALSE									
A34	T5	A34T5	8	196274	146228622	0,504	-0,010288144	1	1
TRUE									
A34	T5	A34T5	9	154795	27556780	0,742	-0,624774011	1	0
FALSE									
A34	T5	A34T5	9	32418237	141016262	0,5	-0,035983405	1	1
TRUE									
A34	T5	A34T5	10	1018585	25888180	0,756	-0,515847269	1	0
FALSE									
A34	T5	A34T5	10	26241025	33552695	0,579	-0,093729299	1	1
FALSE									
A34	T5	A34T5	10	35320355	37505192	0,781	-0,760683112	1	0
FALSE									
A34	T5	A34T5	10	38344700	43678796	0,523	-0,397884877	1	1
TRUE									
A34	T5	A34T5	10	43695049	45958881	0,739	-0,509425291	1	0
FALSE									
A34	T5	A34T5	10	46965018	47000146	0,527	-0,592240173	1	1
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A34	T5	A34T5	10	47667380	135381276	0,756	-0,62397159	1	0
FALSE									
A34	T5	A34T5	11	193865	294537	0,725	0,23248972	2	1
TRUE									
A34	T5	A34T5	11	372157	134856661	0,505	0,051724918	1	1
TRUE									
A34	T5	A34T5	12	250239	133796033	0,504	-0,013094857	1	1
TRUE									
A34	T5	A34T5	13	19600475	115064542	0,504	0,043131792	1	1
TRUE									
A34	T5	A34T5	14	19889910	107178965	0,503	0,07165982	1	1
TRUE									
A34	T5	A34T5	15	20446043	31453147	0,5	-0,007994401	1	1
TRUE									
A34	T5	A34T5	15	31779838	59981590	0,701	-0,458563736	1	0
FALSE									

A34	T5	A34T5	15	60644074	102312835	0,505	0,054869307	1	1 TRUE
A34	T5	A34T5	16	129531	90161231	0,5	-0,115830825	1	1 TRUE
A34	T5	A34T5	17	171098	81050982	0,5	-0,025512703	1	1 TRUE
A34	T5	A34T5	18	203081	77805856	0,5055	0,041982748	1	1 TRUE
A34	T5	A34T5	19	288062	59022697	0,5	-0,148038543	1	1 TRUE
A34	T5	A34T5	20	138125	35467713	0,5	-0,021559771	1	1 TRUE
A34	T5	A34T5	20	35559352	36612084	0,96	3,881490263	28	1 TRUE
A34	T5	A34T5	20	36841756	62903550	0,5	-0,072509356	1	1 TRUE
A34	T5	A34T5	21	10793925	47976203	0,507	-0,025266502	1	1 TRUE
A34	T5	A34T5	22	17054291	51207180	0,5	-0,073564367	1	1 TRUE
A34	T6	A34T6	1	907609	1585642	0,5	-0,296866285	1	1 TRUE
A34	T6	A34T6	1	1633004	1635193	0,5	-3,370303425	0	0 TRUE
A34	T6	A34T6	1	1635565	16382834	0,507	-0,115217611	1	1 TRUE
A34	T6	A34T6	1	16385248	16950449	0,5	-2,651411426	0	0 TRUE
A34	T6	A34T6	1	16974637	203317204	0,5	-0,001328462	1	1 TRUE
A34	T6	A34T6	1	203766827	204516025	0,969	4,127903826	45	1 TRUE
A34	T6	A34T6	1	204915347	249107414	0,5	0,00224944	1	1 TRUE
A34	T6	A34T6	2	224970	70162534	0,5	-0,008041853	1	1 TRUE
A34	T6	A34T6	2	70677994	91809385	0,803	-0,576907335	1	0 TRUE
A34	T6	A34T6	2	95537330	242842568	0,5	-0,017556802	1	1 TRUE
A34	T6	A34T6	3	361508	197402254	0,5	0,003921585	1	1 TRUE
A34	T6	A34T6	4	60400	49063872	0,504	-0,047343406	1	1 TRUE
A34	T6	A34T6	4	52714511	55593464	0,7185	0,670384714	3	1 TRUE

A34	T6	A34T6	4	55946171	190395259	0,5	0,047863588	1	1
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A34	T6	A34T6	5	163205	180665998	0,5	0,071165056	1	1
TRUE									
A34	T6	A34T6	6	335251	170887693	0,5	-0,030276808	1	1
TRUE									
A34	T6	A34T6	7	296739	11419378	0,705	0,557699992	3	1
FALSE									
A34	T6	A34T6	7	11464297	24325009	0,631	0,427856082	2	1
TRUE									
A34	T6	A34T6	7	24844080	54621692	0,6865	0,704317288	3	1
FALSE									
A34	T6	A34T6	7	55214348	55229255	0,98	4,187194678	48	1
TRUE									
A34	T6	A34T6	7	55780176	158827326	0,6935	0,636336869	3	1
FALSE									
A34	T6	A34T6	8	196274	146228622	0,503	-0,027845402	1	1
TRUE									
A34	T6	A34T6	9	154795	27556780	0,792527765	-0,772061015	1	
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A34	T6	A34T6	9	32418237	141016262	0,504	-0,048365296	1	1
TRUE									
A34	T6	A34T6	10	1018585	25888180	0,8035	-0,675440879	1	0
TRUE									
A34	T6	A34T6	10	26241025	33552695	0,5745	-0,096387991	1	1
FALSE									
A34	T6	A34T6	10	35320355	37505192	0,784062505	-0,829756509	1	
0	TRUE								
A34	T6	A34T6	10	38344700	43695049	0,512	-0,280688548	1	1
TRUE									
A34	T6	A34T6	10	44340865	45958881	0,758	-0,665669832	1	0
TRUE									
A34	T6	A34T6	10	46965018	47000146	0,534	-0,884281512	0	0
TRUE									
A34	T6	A34T6	10	47667380	135381276	0,806	-0,702130882	1	0
TRUE									
A34	T6	A34T6	11	193865	134856661	0,505	0,026617466	1	1
TRUE									
A34	T6	A34T6	12	250239	133796033	0,502	-0,011081271	1	1
TRUE									
A34	T6	A34T6	13	19600475	115064542	0,5	0,023472373	1	1
TRUE									
A34	T6	A34T6	14	19889910	107178965	0,5	0,066357604	1	1
TRUE									
A34	T6	A34T6	15	20446043	31779838	0,509	-0,066476635	1	1
TRUE									

A34	T6	A34T6	15	31793930	59981590	0,782	-0,589984005	1	0 FALSE
A34	T6	A34T6	15	60644074	102312835	0,5	0,04576545	1	1 TRUE
A34	T6	A34T6	16	129531	90161231	0,5	-0,105086031	1	1 TRUE
A34	T6	A34T6	17	171098	81050982	0,5	-0,01869474	1	1 TRUE
A34	T6	A34T6	18	203081	77805856	0,5	0,025268006	1	1 TRUE
A34	T6	A34T6	19	288062	59022697	0,5	-0,110588474	1	1 TRUE
A34	T6	A34T6	20	138125	35467713	0,5	-0,02556477	1	1 TRUE
A34	T6	A34T6	20	35559352	36612084	0,97	4,150399965	45	1 TRUE
A34	T6	A34T6	20	36841756	62903550	0,5	-0,063186955	1	1 TRUE
A34	T6	A34T6	21	10793925	47976203	0,503	-0,037582804	1	1 TRUE
A34	T6	A34T6	22	17054291	51207180	0,5	-0,060909815	1	1 TRUE
A44	M	A44M	1	1563789	248814052	0,5	-0,042972375	1	1 TRUE
A44	M	A44M	2	675831	242814463	0,5	-0,037889733	1	1 TRUE
A44	M	A44M	3	239347	197765432	0,5	-0,023676495	1	1 TRUE
A44	M	A44M	4	47658	190395259	0,505	-0,040397262	1	1 TRUE
A44	M	A44M	5	140532	180661256	0,505	-0,04074769	1	1 TRUE
A44	M	A44M	6	203722	29856347	0,503	-0,007091312	1	1 TRUE
A44	M	A44M	6	29856427	33053728	0,505	-0,074702756	1	1 TRUE
A44	M	A44M	6	33053737	33053971	0,6815	-0,197056003	1	0 FALSE
A44	M	A44M	6	33054046	170632383	0,506	-0,046474494	1	1 TRUE
A44	M	A44M	7	228930	158827401	0,5	-0,01340634	1	1 TRUE
A44	M	A44M	8	195347	146056279	0,5	-0,035272335	1	1 TRUE
A44	M	A44M	9	154933	141069927	0,5	-0,037830353	1	1 TRUE

A44	M	A44M	10	285200	51582686	0,5	-0,035550394	1	1
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A44	M	A44M	10	51620231	51620499	0,875	-0,917013216	1	0
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A44	M	A44M	10	51623190	135271764	0,5	-0,027999311	1	1
TRUE									
A44	M	A44M	11	193865	134251777	0,5	-0,025083784	1	1
TRUE									
A44	M	A44M	12	247900	32945769	0,5095	-0,066413605	1	1
TRUE									
A44	M	A44M	12	39997598	133324600	0,5	-0,004704174	1	1
TRUE									
A44	M	A44M	13	19042463	115091399	0,506	-0,044486774	1	1
TRUE									
A44	M	A44M	14	19400419	107283156	0,5	-0,045203035	1	1
TRUE									
A44	M	A44M	15	20170449	102312835	0,5035	-0,058403309	1	1
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A44	M	A44M	16	115041	90050880	0,5	0,012496504	1	1
TRUE									
A44	M	A44M	17	177359	81052423	0,5	-0,01040917	1	1
TRUE									
A44	M	A44M	18	196829	77659561	0,5	-0,073871413	1	1
TRUE									
A44	M	A44M	19	373897	59082368	0,5	0,041411961	1	1
TRUE									
A44	M	A44M	20	207889	62903830	0,5	-0,038581426	1	1
TRUE									
A44	M	A44M	21	10624139	48078611	0,5	-0,029270366	1	1
TRUE									
A44	M	A44M	22	16157883	51171497	0,5	-0,024235809	1	1
TRUE									
A44	S	A44S	1	1563789	248814052	0,5	-0,022171402	1	1
TRUE									
A44	S	A44S	2	675831	242814463	0,504	-0,014591875	1	1
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A44	S	A44S	3	239347	197765432	0,504	-0,008848574	1	1
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A44	S	A44S	4	47658	190395259	0,5	-0,028159589	1	1
TRUE									
A44	S	A44S	5	140532	180661256	0,5	-0,038101924	1	1
TRUE									
A44	S	A44S	6	203722	170632383	0,5	-0,036655762	1	1
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A44	S	A44S	7	228930	158827401	0,5005	0,013719948	1	1
TRUE									

A44	S	A44S	8	195347	146056279	0,5	-0,026262773	1	1
TRUE									
A44	S	A44S	9	154933	141069927	0,5	-0,014261308	1	1
TRUE									
A44	S	A44S	10	285200	135271764	0,503	-0,033236595	1	1
TRUE									
A44	S	A44S	11	193865	134251777	0,502	-0,014374646	1	1
TRUE									
A44	S	A44S	12	247900	32945769	0,5065	-0,038506502	1	1
TRUE									
A44	S	A44S	12	39997598	133324600	0,5	-0,00776582	1	1
TRUE									
A44	S	A44S	13	19042463	115091399	0,5	-0,033005009	1	1
TRUE									
A44	S	A44S	14	19400419	107283156	0,5	-0,029034563	1	1
TRUE									
A44	S	A44S	15	20170449	102312835	0,5	-0,038944566	1	1
TRUE									
A44	S	A44S	16	115041	90050880	0,504	0,027651501	1	1
TRUE									
A44	S	A44S	17	177359	81052423	0,5	0,015644454	1	1
TRUE									
A44	S	A44S	18	196829	77659561	0,5	-0,071504234	1	1
TRUE									
A44	S	A44S	19	373897	59082368	0,5	0,074398827	1	1
TRUE									
A44	S	A44S	20	207889	62903830	0,5	-0,006862614	1	1
TRUE									
A44	S	A44S	21	10624139	48078611	0,5	-0,032461374	1	1
TRUE									
A44	S	A44S	22	16157883	17076273	0,68	0,010437511	2	1
TRUE									
A44	S	A44S	22	17131416	51171497	0,5	-0,014503327	1	1
TRUE									
A44	T1	A44T1	1	1563789	4772053	0,5	0,097250296	1	1
TRUE									
A44	T1	A44T1	1	4847594	6947717	0,71	-0,570922027	1	0
TRUE									
A44	T1	A44T1	1	7723588	248814052	0,5	-0,060005948	1	1
TRUE									
A44	T1	A44T1	2	675831	242814463	0,5	-0,047703884	1	1
TRUE									
A44	T1	A44T1	3	239347	197765432	0,5	-0,038070247	1	1
TRUE									
A44	T1	A44T1	4	47658	980464	0,678	-0,41739074	1	0
FALSE									

A44	T1	A44T1	4	982852	190395259	0,5	-0,049389226	1	1
	TRUE								
A44	T1	A44T1	5	140532	180661256	0,5	-0,054228292	1	1
	TRUE								
A44	T1	A44T1	6	203722	31324025	0,5	-0,038081726	1	1
	TRUE								
A44	T1	A44T1	6	31324200	31324830	0,7325	-0,228835162	1	0
	TRUE								
A44	T1	A44T1	6	31324847	32487038	0,5	0,065660473	1	1
	TRUE								
A44	T1	A44T1	6	32487054	32487123	0,757	0,279186848	2	0
	TRUE								
A44	T1	A44T1	6	32487294	33053092	0,504	-0,103830462	1	1
	TRUE								
A44	T1	A44T1	6	33053477	33054074	0,7	-0,202471029	1	0
	TRUE								
A44	T1	A44T1	6	33071591	160241440	0,504	-0,050464647	1	1
	TRUE								
A44	T1	A44T1	6	160445793	160969738	0,702	-0,495918278	1	0
	TRUE								
A44	T1	A44T1	6	161132146	170632383	0,5	-0,017476142	1	1
	TRUE								
A44	T1	A44T1	7	228930	158827401	0,611	0,344716034	2	1
	TRUE								
A44	T1	A44T1	8	195347	146056279	0,5	-0,035709488	1	1
	TRUE								
A44	T1	A44T1	9	154933	33750748	0,689	-0,570678181	1	0
	FALSE								
A44	T1	A44T1	9	34089395	141069927	0,505	-0,013175857	1	1
	TRUE								
A44	T1	A44T1	10	285200	45672429	0,697	-0,525623455	1	0
	FALSE								
A44	T1	A44T1	10	45689237	47000239	0,506	-0,645952359	0	0
	TRUE								
A44	T1	A44T1	10	47605468	135271764	0,7	-0,500175202	1	0
	FALSE								
A44	T1	A44T1	11	193865	134251777	0,508	-0,015473558	1	1
	TRUE								
A44	T1	A44T1	12	247900	3768705	0,787	-0,03729967	2	0
	FALSE								
A44	T1	A44T1	12	3948718	133324600	0,506	-0,028153981	1	1
	TRUE								
A44	T1	A44T1	13	19042463	115091399	0,504	-0,123786429	1	1
	TRUE								
A44	T1	A44T1	14	19400419	74441684	0,5	-0,047303644	1	1
	TRUE								

A44	T1	A44T1	14	74500585	74512698	0,571	-0,315549901	1	1	TRUE
A44	T1	A44T1	14	74514674	107283156	0,5	-0,041285763	1	1	TRUE
A44	T1	A44T1	15	20170449	22016259	0,522	-0,117075689	1	1	TRUE
A44	T1	A44T1	15	22319166	102312835	0,5	-0,050861772	1	1	TRUE
A44	T1	A44T1	16	115041	90050880	0,5	0,027149966	1	1	TRUE
A44	T1	A44T1	17	177359	14673411	0,5	0,033993948	1	1	TRUE
A44	T1	A44T1	17	15134175	21117589	0,688	-0,466517511	1	0	FALSE
A44	T1	A44T1	17	21312542	22214959	0,5	-0,464161883	1	1	TRUE
A44	T1	A44T1	17	25308787	39551763	0,695	-0,55314438	1	0	FALSE
A44	T1	A44T1	17	39578810	81052423	0,5	0,021948007	1	1	TRUE
A44	T1	A44T1	18	196829	77659561	0,5	-0,102171153	1	1	TRUE
A44	T1	A44T1	19	373897	59082368	0,611	0,433086281	2	1	TRUE
A44	T1	A44T1	20	207889	62903830	0,612	0,321061314	2	1	TRUE
A44	T1	A44T1	21	10624139	48078611	0,5	-0,0172864	1	1	TRUE
A44	T1	A44T1	22	16157883	17131416	0,538	-0,261026308	1	1	TRUE
A44	T1	A44T1	22	17156061	51171497	0,701	-0,455930835	1	0	FALSE
A44	T2	A44T2	1	1563789	248814052	0,5	-0,040635608	1	1	TRUE
A44	T2	A44T2	2	675831	242814463	0,506	-0,038558484	1	1	TRUE
A44	T2	A44T2	3	239347	197765432	0,5	-0,026882812	1	1	TRUE
A44	T2	A44T2	4	47658	190395259	0,5	-0,021711812	1	1	TRUE
A44	T2	A44T2	5	140532	180661256	0,5	-0,037080382	1	1	TRUE
A44	T2	A44T2	6	203722	31324516	0,503	0,024088893	1	1	TRUE
A44	T2	A44T2	6	31324547	31324604	0,725821876	0,250445866	3	0	TRUE

A44	T2	A44T2	6	31324666	32487038	0,5	0,032518399	1	1
TRUE									
A44	T2	A44T2	6	32487054	32489672	0,654054728	-0,084984491	2	
0	FALSE								
A44	T2	A44T2	6	32489744	33053740	0,538	-0,040438763	1	1
FALSE									
A44	T2	A44T2	6	33053780	33054074	0,647044474	-0,113927074	2	
0	TRUE								
A44	T2	A44T2	6	33071591	170632383	0,506	-0,036090908	1	1
TRUE									
A44	T2	A44T2	7	228930	158827401	0,57	0,207538862	2	1
TRUE									
A44	T2	A44T2	8	195347	146056279	0,5	-0,006575762	1	1
TRUE									
A44	T2	A44T2	9	154933	34093274	0,596	-0,301226997	1	0
TRUE									
A44	T2	A44T2	9	34096873	141069927	0,5	-0,02753593	1	1
TRUE									
A44	T2	A44T2	10	285200	133107496	0,593	-0,275853437	1	0
TRUE									
A44	T2	A44T2	10	133608210	133608292	0,670952936	-0,012734618	2	
0	TRUE								
A44	T2	A44T2	10	133748121	135271764	0,6055	-0,275134018	1	0
TRUE									
A44	T2	A44T2	11	193865	134251777	0,5	-0,021109213	1	1
TRUE									
A44	T2	A44T2	12	247900	3768705	0,660203926	-0,059109851	2	
0	TRUE								
A44	T2	A44T2	12	3948718	133324600	0,5	-0,021291253	1	1
TRUE									
A44	T2	A44T2	13	19042463	115091399	0,5	-0,033441724	1	1
TRUE									
A44	T2	A44T2	14	19400419	107283156	0,505	-0,031637082	1	1
TRUE									
A44	T2	A44T2	15	20170449	102312835	0,5	-0,069709097	1	1
TRUE									
A44	T2	A44T2	16	115041	90050880	0,5	0,016355088	1	1
TRUE									
A44	T2	A44T2	17	177359	15154966	0,5	0,025694464	1	1
TRUE									
A44	T2	A44T2	17	15406197	39620399	0,586	-0,289435262	1	0
FALSE									
A44	T2	A44T2	17	39622068	81052423	0,508	0,011546491	1	1
TRUE									
A44	T2	A44T2	18	196829	77659561	0,5	-0,074465604	1	1
TRUE									

A44	T2	A44T2	19	373897	59082368	0,57	0,255230231	2	1	TRUE
A44	T2	A44T2	20	207889	62903830	0,57	0,171762897	2	1	TRUE
A44	T2	A44T2	21	10624139	48078611	0,5	-0,01325936	1	1	TRUE
A44	T2	A44T2	22	16157883	51171497	0,599	-0,286167962	1	0	TRUE
A44	T3	A44T3	1	1563789	248814052	0,506	-0,048353641	1	1	TRUE
A44	T3	A44T3	2	675831	242814463	0,504	-0,060454428	1	1	TRUE
A44	T3	A44T3	3	239347	197765432	0,5	-0,04962555	1	1	TRUE
A44	T3	A44T3	4	47658	190395259	0,504	-0,080965881	1	1	TRUE
A44	T3	A44T3	5	140532	180661256	0,5	-0,069395358	1	1	TRUE
A44	T3	A44T3	6	203722	29893293	0,509	-0,055845808	1	1	TRUE
A44	T3	A44T3	6	29893461	29911154	0,582570504	-0,161304821	1	0	FALSE
A44	T3	A44T3	6	29911190	170632383	0,507	-0,050901636	1	1	TRUE
A44	T3	A44T3	7	228930	158827401	0,5075	0,147779188	2	2	TRUE
A44	T3	A44T3	8	195347	146056279	0,5	-0,032746241	1	1	TRUE
A44	T3	A44T3	9	154933	33613986	0,53	-0,294687626	0	0	FALSE
A44	T3	A44T3	9	33625082	141069927	0,5	-0,014496935	1	1	TRUE
A44	T3	A44T3	10	285200	135271764	0,517	-0,230080508	0	0	FALSE
A44	T3	A44T3	11	193865	134251777	0,5	-0,01999059	1	1	TRUE
A44	T3	A44T3	12	247900	3768705	0,599852979	-0,100302442	2	0	TRUE
A44	T3	A44T3	12	3948718	133324600	0,5	-0,053123931	1	1	TRUE
A44	T3	A44T3	13	19042463	19727724	0,560044843	-0,237128757	1	0	TRUE
A44	T3	A44T3	13	19748344	115091399	0,5	-0,232176743	0	0	TRUE
A44	T3	A44T3	14	19400419	107283156	0,5	-0,036967283	1	1	TRUE

A44	T3	A44T3	15	20170449	102312835	0,504	-0,045251949	1	1 TRUE
A44	T3	A44T3	16	115041	90050880	0,5	0,040213363	1	1 TRUE
A44	T3	A44T3	17	177359	14095566	0,5	0,040986932	1	1 TRUE
A44	T3	A44T3	17	14673411	38348616	0,562	-0,188300009	1	0 TRUE
A44	T3	A44T3	17	38609187	81052423	0,5	0,02296327	1	1 TRUE
A44	T3	A44T3	18	196829	77659561	0,5	-0,109983256	1	1 TRUE
A44	T3	A44T3	19	373897	59082368	0,5	0,244806079	2	2 TRUE
A44	T3	A44T3	20	207889	62903830	0,511	0,158580275	2	2 FALSE
A44	T3	A44T3	21	10624139	48078611	0,5	-0,021948935	1	1 TRUE
A44	T3	A44T3	22	16157883	51171497	0,5685	-0,14823684	1	0 TRUE
A44	T5	A44T5	1	1563789	248814052	0,5	-0,027843144	1	1 TRUE
A44	T5	A44T5	2	675831	242814463	0,5	-0,022770425	1	1 TRUE
A44	T5	A44T5	3	239347	197765432	0,5	-0,011982435	1	1 TRUE
A44	T5	A44T5	4	47658	190395259	0,5	-0,013790654	1	1 TRUE
A44	T5	A44T5	5	140532	180661256	0,5	-0,017690111	1	1 TRUE
A44	T5	A44T5	6	203722	32339647	0,505	-0,003534448	1	1 TRUE
A44	T5	A44T5	6	32369488	32489963	0,641	-0,112156475	1	1 FALSE
A44	T5	A44T5	6	32497943	170632383	0,507	-0,036231521	1	1 TRUE
A44	T5	A44T5	7	228930	158827401	0,5	0,075720605	1	1 TRUE
A44	T5	A44T5	8	195347	146056279	0,5	-0,016798216	1	1 TRUE
A44	T5	A44T5	9	154933	141069927	0,5	-0,036736946	1	1 TRUE
A44	T5	A44T5	10	285200	135271764	0,5	-0,096225187	1	1 TRUE
A44	T5	A44T5	11	193865	134251777	0,5	-0,015959239	1	1 TRUE

A44	T5	A44T5	12	247900	32945769	0,508	-0,057275986	1	1 TRUE
A44	T5	A44T5	12	39997598	133324600	0,5	0,001960039	1	1 TRUE
A44	T5	A44T5	13	19042463	115091399	0,5	-0,005903223	1	1 TRUE
A44	T5	A44T5	14	19400419	107283156	0,5075	-0,026086475	1	1 TRUE
A44	T5	A44T5	15	20170449	102312835	0,5	-0,033725601	1	1 TRUE
A44	T5	A44T5	16	115041	32626855	0,5	0,031845353	1	1 TRUE
A44	T5	A44T5	16	33413927	33413957	0,773	-0,16700353	1	0 TRUE
A44	T5	A44T5	16	34257013	90050880	0,5	0,010623059	1	1 TRUE
A44	T5	A44T5	17	177359	81052423	0,5	-0,006810207	1	1 TRUE
A44	T5	A44T5	18	196829	77659561	0,5	-0,053159782	1	1 TRUE
A44	T5	A44T5	19	373897	59082368	0,5	0,130639089	1	1 TRUE
A44	T5	A44T5	20	207889	62903830	0,5	0,056552389	1	1 TRUE
A44	T5	A44T5	21	10624139	48078611	0,505	-0,019021417	1	1 TRUE
A44	T5	A44T5	22	16157883	51171497	0,5	-0,073379663	1	1 TRUE
SP28	recurrent_M	SP28_recurrent_M	1	808928	248813901	0,5	-0,013669518	1	1 TRUE
SP28	recurrent_M	SP28_recurrent_M	2	173150	242814463	0,505	0,012613663	1	1 TRUE
SP28	recurrent_M	SP28_recurrent_M	3	361508	197581147	0,5	-0,0052783	1	1 TRUE
SP28	recurrent_M	SP28_recurrent_M	4	60303	190905235	0,5	0,006529089	1	1 TRUE
SP28	recurrent_M	SP28_recurrent_M	5	163266	180670470	0,5	0,012421498	1	1 TRUE
SP28	recurrent_M	SP28_recurrent_M	6	335424	31237727	0,5	0,003224272	1	1 TRUE
SP28	recurrent_M	SP28_recurrent_M	6	31237767	31238147	0,706	0,021485957	2	1 FALSE
SP28	recurrent_M	SP28_recurrent_M	6	31238297	32546703	0,5	-0,019043974	1	1 TRUE
SP28	recurrent_M	SP28_recurrent_M	6	32546743	32549331	0,7	0,466609672	2	1 FALSE

SP28	recurrent_M	SP28_recurrent_M	6	32549340	33048348	0,569	-0,005636757	1	1	FALSE
SP28	recurrent_M	SP28_recurrent_M	6	33048599	33052958	0,688	0,216896792	2	1	TRUE
SP28	recurrent_M	SP28_recurrent_M	6	33052986	170892848	0,5	0,006754585	1	1	TRUE
SP28	recurrent_M	SP28_recurrent_M	7	296739	159024799	0,5	-0,013769875	1	1	TRUE
SP28	recurrent_M	SP28_recurrent_M	8	182949	146222122	0,5	0,016106563	1	1	TRUE
SP28	recurrent_M	SP28_recurrent_M	9	154795	141070950	0,5	-0,00712782	1	1	TRUE
SP28	recurrent_M	SP28_recurrent_M	10	1052950	135279979	0,5	-0,001562733	1	1	TRUE
SP28	recurrent_M	SP28_recurrent_M	11	193112	134856661	0,5	-0,016602508	1	1	TRUE
SP28	recurrent_M	SP28_recurrent_M	12	310901	133808129	0,5	-0,012454859	1	1	TRUE
SP28	recurrent_M	SP28_recurrent_M	13	19042581	114323997	0,5035	0,018493788	1	1	TRUE
SP28	recurrent_M	SP28_recurrent_M	14	19411738	107283160	0,5	0,005759296	1	1	TRUE
SP28	recurrent_M	SP28_recurrent_M	15	20169854	102313869	0,5	-0,013132091	1	1	TRUE
SP28	recurrent_M	SP28_recurrent_M	16	97610	90142087	0,5	-0,063592576	1	1	TRUE
SP28	recurrent_M	SP28_recurrent_M	17	6115	81052423	0,502	-0,071550762	1	1	TRUE
SP28	recurrent_M	SP28_recurrent_M	18	196829	77896242	0,5	0,015525484	1	1	TRUE
SP28	recurrent_M	SP28_recurrent_M	19	367089	59010819	0,5	-0,108533768	1	1	TRUE
SP28	recurrent_M	SP28_recurrent_M	20	76962	62959184	0,5	-0,018716718	1	1	TRUE
SP28	recurrent_M	SP28_recurrent_M	21	9650104	11186346	0,582	0,077231359	1	1	FALSE
SP28	recurrent_M	SP28_recurrent_M	21	14433284	48083526	0,506	0,005204273	1	1	TRUE
SP28	recurrent_M	SP28_recurrent_M	22	16255826	51065831	0,5	-0,069367822	1	1	TRUE
SP28	recurrent_S	SP28_recurrent_S	1	808928	147287992	0,507	0,030584765	1	1	TRUE
SP28	recurrent_S	SP28_recurrent_S	1	148342446	149648627	0,678	-0,114242534	1	0	TRUE
SP28	recurrent_S	SP28_recurrent_S	1	149648696	248813901	0,509	0,050686339	1	1	TRUE

SP28	recurrent_S	SP28_recurrent_S	2	173150	209358027	0,505	-0,137038733	1	1	TRUE	
SP28	recurrent_S	SP28_recurrent_S	2	210010065	210010136	0,562242793	-0,822774491	0	0	TRUE	
SP28	recurrent_S	SP28_recurrent_S	2	210043728	242814463	0,5	-0,148281545	1	1	TRUE	
SP28	recurrent_S	SP28_recurrent_S	3	361508	197581147	0,5	0,050277215	1	1	TRUE	
SP28	recurrent_S	SP28_recurrent_S	4	60303	190905235	0,504	-0,066921899	1	1	TRUE	
SP28	recurrent_S	SP28_recurrent_S	5	163266	180670470	0,573	-0,048281024	1	1	FALSE	
SP28	recurrent_S	SP28_recurrent_S	6	335424	31237727	0,505	0,046922204	1	1	TRUE	
SP28	recurrent_S	SP28_recurrent_S	6	31237767	31238297	0,692	-0,013108958	1	0	TRUE	
SP28	recurrent_S	SP28_recurrent_S	6	31238308	32525928	0,5	0,012453931	1	1	TRUE	
SP28	recurrent_S	SP28_recurrent_S	6	32546696	32546935	0,7255	0,442552417	3	1	FALSE	
SP28	recurrent_S	SP28_recurrent_S	6	32546940	33095615	0,5845	0,066086829	2	1	FALSE	
SP28	recurrent_S	SP28_recurrent_S	6	33095636	170892848	0,5	0,044326112	1	1	TRUE	
SP28	recurrent_S	SP28_recurrent_S	7	296739	159024799	0,594	0,059972885	2	1	FALSE	
SP28	recurrent_S	SP28_recurrent_S	8	182949	146222122	0,5	0,105843425	1	1	TRUE	
SP28	recurrent_S	SP28_recurrent_S	9	154795	141070950	0,5	0,037150834	1	1	TRUE	
SP28	recurrent_S	SP28_recurrent_S	10	1052950	51124153	0,711	-0,186541301	1	0	FALSE	
SP28	recurrent_S	SP28_recurrent_S	10	51532621	51633027	0,538	-0,339614192	1	1	TRUE	
SP28	recurrent_S	SP28_recurrent_S	10	51785728	135279979	0,716433627	-0,196330024	1	0	FALSE	
SP28	recurrent_S	SP28_recurrent_S	11	193112	59830198	0,5	0,275346088	1	1	TRUE	
SP28	recurrent_S	SP28_recurrent_S	11	59860178	63072310	0,691849345	-0,316279419	1	0	FALSE	
SP28	recurrent_S	SP28_recurrent_S	11	63129782	64950970	0,508	-0,044585421	1	1	TRUE	
SP28	recurrent_S	SP28_recurrent_S	11	64972354	134856661	0,683	-0,2890111	1	0	TRUE	
SP28	recurrent_S	SP28_recurrent_S	12	310901	11244941	0,57	-0,137024199	1	1	FALSE	

SP28	recurrent_S	SP28_recurrent_S	12	11338539	34175508	0,5	0,026353136
1	1	TRUE					
SP28	recurrent_S	SP28_recurrent_S	12	37969194	133808129	0,564	-0,11422155
1	1	FALSE					
SP28	recurrent_S	SP28_recurrent_S	13	19042581	42876290	0,505	0,165064311
1	1	TRUE					
SP28	recurrent_S	SP28_recurrent_S	13	43180503	95230412	0,684	-0,28561787
1	0	TRUE					
SP28	recurrent_S	SP28_recurrent_S	13	95275576	114323997	0,507	0,114027247
1	1	TRUE					
SP28	recurrent_S	SP28_recurrent_S	14	19411738	107283160	0,5	0,049949032
1	1	TRUE					
SP28	recurrent_S	SP28_recurrent_S	15	20169854	22692271	0,607	-0,290927489
1	0	FALSE					
SP28	recurrent_S	SP28_recurrent_S	15	22788922	102313869	0,681	-0,310055758
1	0	TRUE					
SP28	recurrent_S	SP28_recurrent_S	16	97610	90142087	0,5	-0,169052845
1	1	TRUE					
SP28	recurrent_S	SP28_recurrent_S	17	6115	2930339	0,76	0,123790436
2	0	TRUE					
SP28	recurrent_S	SP28_recurrent_S	17	2965929	2966308	0,51	-0,032287907
1	1	TRUE					
SP28	recurrent_S	SP28_recurrent_S	17	3144286	20945887	0,767891883	0,092559463
2	0	TRUE					
SP28	recurrent_S	SP28_recurrent_S	17	21194769	81052423	0,5	0,114558818
1	1	TRUE					
SP28	recurrent_S	SP28_recurrent_S	18	196829	77896242	0,5	0,056464775
1	1	TRUE					
SP28	recurrent_S	SP28_recurrent_S	19	367089	53612720	0,667	0,174135445
2	1	FALSE					
SP28	recurrent_S	SP28_recurrent_S	19	53612989	59010819	0,649	0,151102047
2	1	FALSE					
SP28	recurrent_S	SP28_recurrent_S	20	76962	62959184	0,591	-0,17425896
1	0	FALSE					
SP28	recurrent_S	SP28_recurrent_S	21	9650104	11186346	0,591	0,030737625
1	0	FALSE					
SP28	recurrent_S	SP28_recurrent_S	21	14433284	48083526	0,506	0,157852634
1	1	TRUE					
SP28	recurrent_S	SP28_recurrent_S	22	16255826	51065831	0,5	0,020542274
1	1	TRUE					
SP28	recurrent_T	SP28_recurrent_T	1	808928	248813901	0,5	0,025667906
1	1	TRUE					
SP28	recurrent_T	SP28_recurrent_T	2	173150	242814463	0,512	-0,124968801
1	1	FALSE					
SP28	recurrent_T	SP28_recurrent_T	3	361508	197581147	0,5	0,046522095
1	1	TRUE					

SP28	recurrent_T	SP28_recurrent_T	4	60303	190905235	0,5045	-0,009753476	1	1	TRUE	
SP28	recurrent_T	SP28_recurrent_T	5	163266	180670470	0,566	-0,083908871	1	1	FALSE	
SP28	recurrent_T	SP28_recurrent_T	6	335424	29855401	0,505	0,055625939	1	1	TRUE	
SP28	recurrent_T	SP28_recurrent_T	6	29855849	29855864	0,715469089	-0,126510968	2	0	TRUE	
SP28	recurrent_T	SP28_recurrent_T	6	29855940	31237723	0,5	-0,041758471	1	1	TRUE	
SP28	recurrent_T	SP28_recurrent_T	6	31237727	31238322	0,667	-0,036985894	1	0	TRUE	
SP28	recurrent_T	SP28_recurrent_T	6	31238372	32522490	0,5	-0,006887214	1	1	TRUE	
SP28	recurrent_T	SP28_recurrent_T	6	32522501	32546953	0,7245	0,287816002	2	0	TRUE	
SP28	recurrent_T	SP28_recurrent_T	6	32548122	32629889	0,505	-0,081587758	1	1	TRUE	
SP28	recurrent_T	SP28_recurrent_T	6	32629904	32634505	0,667	-0,071775704	1	0	TRUE	
SP28	recurrent_T	SP28_recurrent_T	6	32713487	114279783	0,503	0,038842098	1	1	TRUE	
SP28	recurrent_T	SP28_recurrent_T	6	116774259	116774616	0,790665671	0,316265501	3	0	TRUE	
SP28	recurrent_T	SP28_recurrent_T	6	116782478	170892848	0,5	0,055408842	1	1	TRUE	
SP28	recurrent_T	SP28_recurrent_T	7	296739	6063283	0,639	0,084837461	2	1	FALSE	
SP28	recurrent_T	SP28_recurrent_T	7	6063674	159024799	0,609	0,142740038	2	1	FALSE	
SP28	recurrent_T	SP28_recurrent_T	8	182949	146222122	0,5	0,036719939	1	1	TRUE	
SP28	recurrent_T	SP28_recurrent_T	9	154795	141070950	0,5	0,012158994	1	1	TRUE	
SP28	recurrent_T	SP28_recurrent_T	10	1052950	135279979	0,684	-0,289579377	1	0	FALSE	
SP28	recurrent_T	SP28_recurrent_T	11	193112	59830198	0,565	0,244386614	2	1	FALSE	
SP28	recurrent_T	SP28_recurrent_T	11	59860178	63072310	0,6765	-0,309253086	1	0	TRUE	
SP28	recurrent_T	SP28_recurrent_T	11	63129782	64972354	0,5	-0,080177249	1	1	TRUE	
SP28	recurrent_T	SP28_recurrent_T	11	64977424	67795353	0,650293642	-0,424069601	1	0	FALSE	
SP28	recurrent_T	SP28_recurrent_T	11	67798381	134856661	0,66	-0,311974643	1	0	TRUE	

SP28	recurrent_T	SP28_recurrent_T	12	310901	133808129	0,5	-0,066337641
1	1	TRUE					
SP28	recurrent_T	SP28_recurrent_T	13	19042581	19950468	0,627	-0,347074778
1	0	FALSE					
SP28	recurrent_T	SP28_recurrent_T	13	19956653	43358176	0,5	0,137390191
1	1	TRUE					
SP28	recurrent_T	SP28_recurrent_T	13	43597977	95034749	0,659	-0,281590604
1	0	TRUE					
SP28	recurrent_T	SP28_recurrent_T	13	95097956	114323997	0,51	0,062777388
1	1	TRUE					
SP28	recurrent_T	SP28_recurrent_T	14	19411738	107283160	0,5	0,044204929
1	1	TRUE					
SP28	recurrent_T	SP28_recurrent_T	15	20169854	22140512	0,531	-0,340429388
1	1	TRUE					
SP28	recurrent_T	SP28_recurrent_T	15	22145552	102313869	0,667	-0,329773731
1	0	TRUE					
SP28	recurrent_T	SP28_recurrent_T	16	97610	90142087	0,5	-0,14275515
1	1	TRUE					
SP28	recurrent_T	SP28_recurrent_T	17	6115	2930339	0,735	0,003335445
2	0	TRUE					
SP28	recurrent_T	SP28_recurrent_T	17	2965929	3144286	0,533	-0,127536746
1	1	TRUE					
SP28	recurrent_T	SP28_recurrent_T	17	3379815	8167600	0,749067021	0,054772336
2	0	TRUE					
SP28	recurrent_T	SP28_recurrent_T	17	8168224	20945887	0,735	-0,034250828
2	0	FALSE					
SP28	recurrent_T	SP28_recurrent_T	17	21194769	81052423	0,5	0,0262627
1	1	TRUE					
SP28	recurrent_T	SP28_recurrent_T	18	196829	77896242	0,5	0,036864229
1	1	TRUE					
SP28	recurrent_T	SP28_recurrent_T	19	367089	59010819	0,625	0,18577287
2	1	FALSE					
SP28	recurrent_T	SP28_recurrent_T	20	76962	62959184	0,51	-0,150311291
1	1	FALSE					
SP28	recurrent_T	SP28_recurrent_T	21	9650104	48083526	0,5	0,075104503
1	1	TRUE					
SP28	recurrent_T	SP28_recurrent_T	22	16255826	51065831	0,5	-0,048904429
1	1	TRUE					
A23	primary_M	A23_primary_M	1	13273	72740634	0,5	0,048955309
2	2	TRUE					
A23	primary_M	A23_primary_M	1	74664149	104076537	0,582984881	-0,232324553
2	0	TRUE					
A23	primary_M	A23_primary_M	1	104084226	248814126	0,5	0,027449327
2	2	TRUE					
A23	primary_M	A23_primary_M	2	45843	243037004	0,5	0,016097206
2	2	TRUE					

A23	primary_M2	A23_primary_M2	3	403288	168269756	0,5	0,012332662
A23	primary_M6	A23_primary_M2	3	168804431	180703663	0,621	0,377447201
A23	primary_M53	A23_primary_M2	3	182681740	184588420	0,894	2,325426212
A23	primary_M2	A23_primary_M2	3	184616504	197837967	0,5	0,050384134
A23	primary_M2	A23_primary_M2	4	195436	190903950	0,5	0,018172373
A23	primary_M2	A23_primary_M2	5	163205	180583043	0,5	0,025661524
A23	primary_M1	A23_primary_M1	6	203722	33048663	0,508	-0,138563225
A23	primary_M3	A23_primary_M0	6	33048686	33053812	0,61344137	-0,12291211
A23	primary_M1	A23_primary_M1	6	33060064	170892848	0,5	-0,092643346
A23	primary_M4	A23_primary_M2	7	295970	53255471	0,5775	0,204574056
A23	primary_M127	A23_primary_M2	7	53930720	56022544	0,954	3,414444989
A23	primary_M4	A23_primary_M2	7	56047572	159053596	0,5635	0,229197543
A23	primary_M2	A23_primary_M2	8	182934	146228622	0,5	-0,001298881
A23	primary_M2	A23_primary_M2	9	214864	141071475	0,505	0,005807276
A23	primary_M2	A23_primary_M0	10	132135	38737254	0,589349848	-0,210134696
A23	primary_M2	A23_primary_M0	10	43315692	93771192	0,5685	-0,195723889
A23	primary_M2	A23_primary_M0	10	93786557	135381592	0,580049312	-0,242444794
A23	primary_M1	A23_primary_M1	11	192997	134252121	0,5	-0,106982619
A23	primary_M2	A23_primary_M2	12	248202	133795960	0,5	0,034110554
A23	primary_M2	A23_primary_M2	13	19059494	115030714	0,5	0,03841216
A23	primary_M2	A23_primary_M2	14	19401146	107178965	0,5	0,018011793
A23	primary_M2	A23_primary_M2	15	20173245	102304498	0,5	0,021913198
A23	primary_M2	A23_primary_M2	16	97610	90133064	0,5	-0,07425844

A23	primary_M 2	2	A23_primary_M 2	TRUE	17	6177	81006629	0,5	0,030321604
A23	primary_M 2	2	A23_primary_M 2	TRUE	18	204780	77926862	0,5	-0,015922866
A23	primary_M 2	2	A23_primary_M 2	TRUE	19	312164	59082605	0,5	0,027127279
A23	primary_M 2	2	A23_primary_M 2	TRUE	20	76962	62903550	0,5	0,036528896
A23	primary_M 3	0	A23_primary_M 2	TRUE	21	9891930	9907416	0,618959177	-0,102170433
A23	primary_M 2	2	A23_primary_M 2	TRUE	21	10862853	48078611	0,5	0,010416835
A23	primary_M 2	2	A23_primary_M 2	TRUE	22	16393311	51219006	0,5	0,027614631
A23	primary_S 2	2	A23_primary_S 2	TRUE	1	13273	72740634	0,5	0,054752312
A23	primary_S 2	0	A23_primary_S 2	TRUE	1	74664149	99753631	0,746771865	-0,564869274
A23	primary_S 2	2	A23_primary_S 2	TRUE	1	100715454	248814126	0,5	0,024026661
A23	primary_S 2	2	A23_primary_S 2	TRUE	2	45843	243037004	0,5	0,014672632
A23	primary_S 2	2	A23_primary_S 2	TRUE	3	403288	171510238	0,505	0,021472492
A23	primary_S 60	2	A23_primary_S 2	TRUE	3	171844787	172099011	0,955	3,436308841
A23	primary_S 2	2	A23_primary_S 2	FALSE	3	172144718	180703663	0,522	-0,127043818
A23	primary_S 74	2	A23_primary_S 2	TRUE	3	182681740	184299167	0,9655	3,718768161
A23	primary_S 4	2	A23_primary_S 2	TRUE	3	184550501	186276393	0,627	0,337928421
A23	primary_S 2	2	A23_primary_S 2	TRUE	3	186314734	197837967	0,5	-0,001275892
A23	primary_S 2	2	A23_primary_S 2	TRUE	4	195436	190903950	0,5	0,009662857
A23	primary_S 2	2	A23_primary_S 2	TRUE	5	163205	180583043	0,5	0,021080752
A23	primary_S 2	2	A23_primary_S 2	TRUE	6	203722	29897259	0,5	-0,029476351
A23	primary_S 2	0	A23_primary_S 2	FALSE	6	29897301	29911240	0,686	-0,347200886
A23	primary_S 2	2	A23_primary_S 2	TRUE	6	29911260	170892848	0,5	0,001551187
A23	primary_S 4	2	A23_primary_S 2	TRUE	7	295970	53255471	0,625	0,428829697

A23	primary_S	A23_primary_S	7	53930720	55780845	0,941	3,23911179	51
2	TRUE							
A23	primary_S	A23_primary_S	7	55991292	57642490	0,792	1,382649292	11
2	TRUE							
A23	primary_S	A23_primary_S	7	63040467	76112060	0,621	0,496106644	4
2	TRUE							
A23	primary_S	A23_primary_S	7	76131645	76131695	0,78909766	-0,301006668	3
0	FALSE							
A23	primary_S	A23_primary_S	7	76132898	159053596	0,625	0,437269181	4
2	TRUE							
A23	primary_S	A23_primary_S	8	182934	146228622	0,506	0,010848146	2
2	TRUE							
A23	primary_S	A23_primary_S	9	214864	24545513	0,5	-0,139766383	2
2	TRUE							
A23	primary_S	A23_primary_S	9	25677933	27567145	0,742720344	-0,587768949	2
0	TRUE							
A23	primary_S	A23_primary_S	9	28863459	44175535	0,5	-0,005445438	2
2	TRUE							
A23	primary_S	A23_primary_S	9	65973404	68433462	0,663	-0,107066003	3
1	TRUE							
A23	primary_S	A23_primary_S	9	69002200	141071475	0,506	0,012421476	2
2	TRUE							
A23	primary_S	A23_primary_S	10	132135	25701341	0,75166698	-0,536707674	2
0	TRUE							
A23	primary_S	A23_primary_S	10	26310403	26994150	0,627	-0,232122264	2
1	FALSE							
A23	primary_S	A23_primary_S	10	27326999	38737254	0,741792705	-0,592961328	2
0	TRUE							
A23	primary_S	A23_primary_S	10	43315692	63964653	0,591	-0,299398166	2
1	TRUE							
A23	primary_S	A23_primary_S	10	64239709	73970451	0,75	-0,502007625	2
0	TRUE							
A23	primary_S	A23_primary_S	10	75556404	77807092	0,514	0,261298103	3
3	TRUE							
A23	primary_S	A23_primary_S	10	79779150	82249108	0,731528639	-0,649199765	2
0	TRUE							
A23	primary_S	A23_primary_S	10	85902394	90034899	0,656	-0,899547427	1
0	TRUE							
A23	primary_S	A23_primary_S	10	90354589	135381592	0,75	-0,541094995	2
0	TRUE							
A23	primary_S	A23_primary_S	11	192997	134252121	0,604	-0,25193671	2
1	TRUE							
A23	primary_S	A23_primary_S	12	248202	133795960	0,5	0,019962785	2
2	TRUE							
A23	primary_S	A23_primary_S	13	19059494	115030714	0,503	0,036953339	2
2	TRUE							

A23	primary_S	A23_primary_S	14	19401146	107178965	0,507	0,014225361
2	2	TRUE					
A23	primary_S	A23_primary_S	15	20173245	102304498	0,5	0,035246944
2	2	TRUE					
A23	primary_S	A23_primary_S	16	97610	90133064	0,589	-0,211368732
2	1	FALSE					
A23	primary_S	A23_primary_S	17	6177	81006629	0,5	0,03951862
2	2	TRUE					
A23	primary_S	A23_primary_S	18	204780	77926862	0,505	0,00492966
2	2	TRUE					
A23	primary_S	A23_primary_S	19	312164	59082605	0,6	-0,210281083
2	1	TRUE					
A23	primary_S	A23_primary_S	20	76962	62903550	0,502	0,024923894
2	2	TRUE					
A23	primary_S	A23_primary_S	21	9891930	48078611	0,5	-0,002972587
2	2	TRUE					
A23	primary_S	A23_primary_S	22	16393311	51219006	0,5	0,053387456
2	2	TRUE					
A23	primary_T	A23_primary_T	1	13273	72740634	0,5	0,032504932
2	2	TRUE					
A23	primary_T	A23_primary_T	1	74664149	99753631	0,753	-0,594331048
2	0	TRUE					
A23	primary_T	A23_primary_T	1	100715454	248814126	0,5	0,00554177
2	2	TRUE					
A23	primary_T	A23_primary_T	2	45843	243037004	0,505	-0,010445404
2	2	TRUE					
A23	primary_T	A23_primary_T	3	403288	168269756	0,5	0,003635093
2	2	TRUE					
A23	primary_T	A23_primary_T	3	168804431	170425956	0,8655	1,807140231
17	2	TRUE					
A23	primary_T	A23_primary_T	3	170797252	178917005	0,611	0,215366557
3	2	FALSE					
A23	primary_T	A23_primary_T	3	178922274	180703663	0,757	0,915563062
8	2	TRUE					
A23	primary_T	A23_primary_T	3	182681740	184766392	0,899	2,211003361
24	2	TRUE					
A23	primary_T	A23_primary_T	3	185635685	197837967	0,5	-0,028464965
2	2	TRUE					
A23	primary_T	A23_primary_T	4	195436	190903950	0,5	-0,012765349
2	2	TRUE					
A23	primary_T	A23_primary_T	5	163205	180583043	0,5	0,006545532
2	2	TRUE					
A23	primary_T	A23_primary_T	6	203722	170892848	0,5	-0,027424967
2	2	TRUE					
A23	primary_T	A23_primary_T	7	295970	53255471	0,6305	0,427207212
4	2	TRUE					

A23	primary_T	A23_primary_T	7	53930720	56022544	0,962		
	3,672188406	71	2	TRUE				
A23	primary_T	A23_primary_T	7	56047572	159053596	0,6275		
	0,427597441	4	2	TRUE				
A23	primary_T	A23_primary_T	8	182934	146228622	0,5	-	
0,006066039	2	2	TRUE					
A23	primary_T	A23_primary_T	9	214864	24545513	0,5	-	
0,140046673	2	2	TRUE					
A23	primary_T	A23_primary_T	9	25677933	27567145	0,719	-	
0,741132557	1	0	FALSE					
A23	primary_T	A23_primary_T	9	28863459	44175535	0,5	-	
0,01660197	2	2	TRUE					
A23	primary_T	A23_primary_T	9	65973404	66455647	0,6325	-	
0,195350092	2	1	TRUE					
A23	primary_T	A23_primary_T	9	66457475	141071475	0,5		
	0,004263455	2	2	TRUE				
A23	primary_T	A23_primary_T	10	132135	25701341	0,7615	-	
0,552544414	2	0	TRUE					
A23	primary_T	A23_primary_T	10	26310403	26534937	0,62	-	
0,24210603	2	1	FALSE					
A23	primary_T	A23_primary_T	10	26559571	38737254	0,75	-	
0,57268752	2	0	TRUE					
A23	primary_T	A23_primary_T	10	43315692	63700245	0,588	-	
0,30436576	2	1	FALSE					
A23	primary_T	A23_primary_T	10	63964653	75556404	0,749	-	
0,606564925	2	0	FALSE					
A23	primary_T	A23_primary_T	10	75671875	77807092	0,51		
	0,17757269	2	2	TRUE				
A23	primary_T	A23_primary_T	10	79779150	82249108	0,740172548		
	-0,703045639	2	0	TRUE				
A23	primary_T	A23_primary_T	10	85902394	88428335	0,508	-	
0,589807045	1	1	TRUE					
A23	primary_T	A23_primary_T	10	88635779	92912588	0,734328559		
	-0,735134922	2	0	FALSE				
A23	primary_T	A23_primary_T	10	92912773	135381592	0,762	-	
0,573993845	2	0	TRUE					
A23	primary_T	A23_primary_T	11	192997	134252121	0,597	-	
0,28790233	2	1	TRUE					
A23	primary_T	A23_primary_T	12	248202	133795960	0,5		
	0,007573605	2	2	TRUE				
A23	primary_T	A23_primary_T	13	19059494	115030714	0,507	-	
0,115762542	2	2	TRUE					
A23	primary_T	A23_primary_T	14	19401146	107178965	0,5		
	0,010978763	2	2	TRUE				
A23	primary_T	A23_primary_T	15	20173245	102304498	0,5		
	0,012436059	2	2	TRUE				

A23	primary_T2	A23_primary_T2	16	97610	90133064	0,5065	-0,202505391
A23	primary_T2	A23_primary_T2	17	6177	81006629	0,5	0,01657154
A23	primary_T2	A23_primary_T2	18	204780	77926862	0,504	-0,012410016
A23	primary_T2	A23_primary_T2	19	312164	59082605	0,5	0,04771544
A23	primary_T2	A23_primary_T2	20	76962	62903550	0,5	0,017515004
A23	primary_T2	A23_primary_T2	21	9891930	48078611	0,502	-0,009818456
A23	primary_T2	A23_primary_T2	22	16393311	51219006	0,506	-0,074019911
SP28	primary_M1	SP28_primary_M1	1	808928	248813901	0,5	-0,000371537
SP28	primary_M1	SP28_primary_M1	2	173150	242814463	0,502	0,017289829
SP28	primary_M1	SP28_primary_M1	3	361508	197581147	0,5	0,012809525
SP28	primary_M1	SP28_primary_M1	4	60303	190905235	0,5	0,035888252
SP28	primary_M1	SP28_primary_M1	5	163266	180670470	0,5	0,016919492
SP28	primary_M1	SP28_primary_M1	6	335424	31237833	0,5	0,003376966
SP28	primary_M2	SP28_primary_M1	6	31237862	31239766	0,632	0,116876804
SP28	primary_M1	SP28_primary_M1	6	31239802	31924327	0,5	-0,035378104
SP28	primary_M1	SP28_primary_M1	6	31926600	32714516	0,5755	0,027650416
SP28	primary_M1	SP28_primary_M1	6	32714592	170892848	0,5	0,02399774
SP28	primary_M1	SP28_primary_M1	7	296739	159024799	0,5	0,007514868
SP28	primary_M1	SP28_primary_M1	8	182949	146222122	0,5	0,025616635
SP28	primary_M1	SP28_primary_M1	9	154795	141070950	0,506	-0,003593571
SP28	primary_M1	SP28_primary_M1	10	1052950	135279979	0,5045	-0,01157027
SP28	primary_M1	SP28_primary_M1	11	193112	134856661	0,5	-0,009454102
SP28	primary_M1	SP28_primary_M1	12	310901	8203273	0,503	-0,070715019

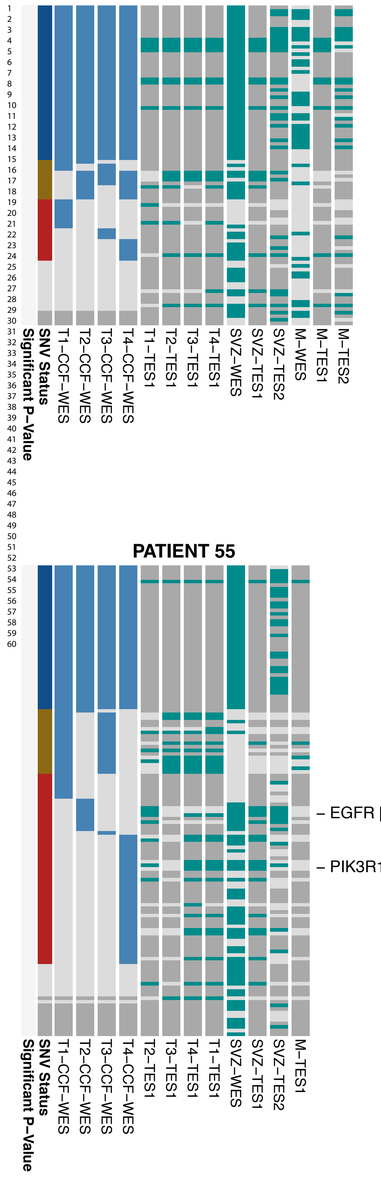
SP28	primary_M	SP28_primary_M	12	8492799	8509576	0,744	-0,31777576
1	1	TRUE					
SP28	primary_M	SP28_primary_M	12	8509668	133808129	0,5	0,004120847
1	1	TRUE					
SP28	primary_M	SP28_primary_M	13	19042581	114323997	0,5015	0,030213101
1	1	TRUE					
SP28	primary_M	SP28_primary_M	14	19411738	107283160	0,5	-0,004108061
1	1	TRUE					
SP28	primary_M	SP28_primary_M	15	20169854	102313869	0,5	-0,007211947
1	1	TRUE					
SP28	primary_M	SP28_primary_M	16	97610	90142087	0,5	-0,050338588
1	1	TRUE					
SP28	primary_M	SP28_primary_M	17	6115	81052423	0,5	-0,062575304
1	1	TRUE					
SP28	primary_M	SP28_primary_M	18	196829	77896242	0,5015	0,023080347
1	1	TRUE					
SP28	primary_M	SP28_primary_M	19	367089	7743159	0,5	-0,128676849
1	1	TRUE					
SP28	primary_M	SP28_primary_M	19	7754942	7755056	0,769	-0,126731082
1	0	FALSE					
SP28	primary_M	SP28_primary_M	19	7755159	59010819	0,503	-0,065501578
1	1	TRUE					
SP28	primary_M	SP28_primary_M	20	76962	62959184	0,5	-0,038576729
1	1	TRUE					
SP28	primary_M	SP28_primary_M	21	9650104	48083526	0,5	0,010527718
1	1	TRUE					
SP28	primary_M	SP28_primary_M	22	16255826	51065831	0,5	-0,068285282
1	1	TRUE					
SP28	primary_S	SP28_primary_S	1	808928	147287992	0,505	-0,029224509
1	1	TRUE					
SP28	primary_S	SP28_primary_S	1	148342446	148902833	0,717	-0,023598749
1	0	FALSE					
SP28	primary_S	SP28_primary_S	1	149648627	248813901	0,5	0,026114229
1	1	TRUE					
SP28	primary_S	SP28_primary_S	2	173150	242814463	0,5	0,022086935
1	1	TRUE					
SP28	primary_S	SP28_primary_S	3	361508	197581147	0,5	0,012702413
1	1	TRUE					
SP28	primary_S	SP28_primary_S	4	60303	190905235	0,503	0,034478274
1	1	TRUE					
SP28	primary_S	SP28_primary_S	5	163266	180670470	0,5	0,015191908
1	1	TRUE					
SP28	primary_S	SP28_primary_S	6	335424	31237727	0,504	0,004132437
1	1	TRUE					
SP28	primary_S	SP28_primary_S	6	31237767	31238308	0,6765	0,027601497
2	1	TRUE					

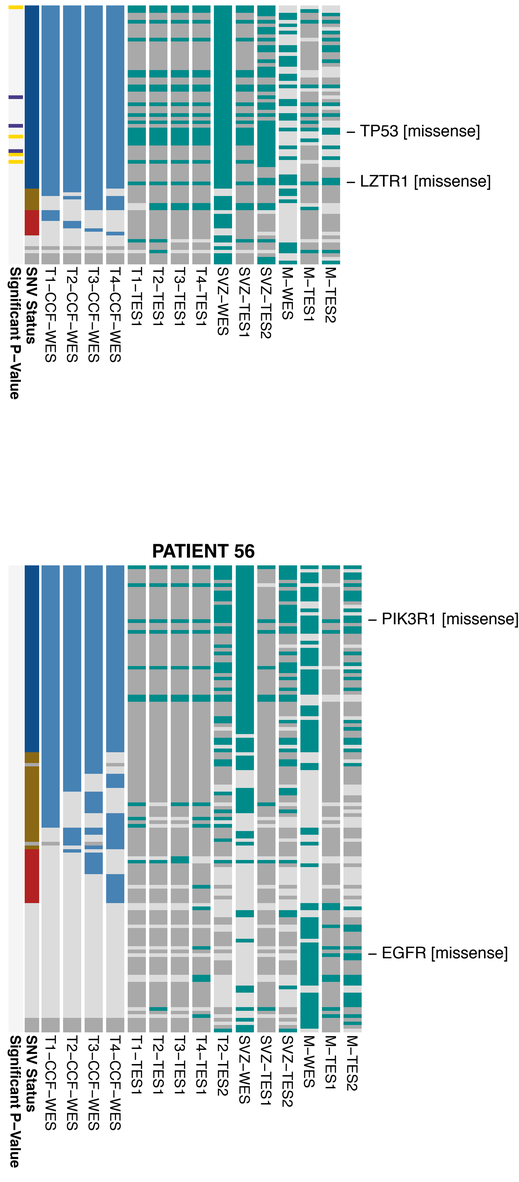
SP28	primary_S	SP28_primary_S	6	31238318	32489642	0,507	-0,000865771	1	1	TRUE
SP28	primary_S	SP28_primary_S	6	32489707	32628001	0,628	-0,036818021	1	1	FALSE
SP28	primary_S	SP28_primary_S	6	32628030	33036630	0,513	0,001732368	1	1	FALSE
SP28	primary_S	SP28_primary_S	6	33036717	33037768	0,6495	0,264528516	2	1	TRUE
SP28	primary_S	SP28_primary_S	6	33043930	170892848	0,5	0,018152218	1	1	TRUE
SP28	primary_S	SP28_primary_S	7	296739	159024799	0,5	-0,004728198	1	1	TRUE
SP28	primary_S	SP28_primary_S	8	182949	146222122	0,505	0,017022579	1	1	TRUE
SP28	primary_S	SP28_primary_S	9	154795	45372293	0,506	0,023631267	1	1	TRUE
SP28	primary_S	SP28_primary_S	9	65595104	141070950	0,5	0,001708899	1	1	TRUE
SP28	primary_S	SP28_primary_S	10	1052950	135279979	0,5	0,003575793	1	1	TRUE
SP28	primary_S	SP28_primary_S	11	193112	134856661	0,5	-0,007932024	1	1	TRUE
SP28	primary_S	SP28_primary_S	12	310901	133808129	0,5	-2,73E-05	1	1	TRUE
SP28	primary_S	SP28_primary_S	13	19042581	114323997	0,504	0,026764251	1	1	TRUE
SP28	primary_S	SP28_primary_S	14	19411738	107283160	0,5	0,005921423	1	1	TRUE
SP28	primary_S	SP28_primary_S	15	20169854	102313869	0,5	-0,004197176	1	1	TRUE
SP28	primary_S	SP28_primary_S	16	97610	90142087	0,5	-0,065855136	1	1	TRUE
SP28	primary_S	SP28_primary_S	17	6115	81052423	0,5	-0,073291896	1	1	TRUE
SP28	primary_S	SP28_primary_S	18	196829	77896242	0,5	0,034432231	1	1	TRUE
SP28	primary_S	SP28_primary_S	19	367089	59010819	0,5	-0,122919503	1	1	TRUE
SP28	primary_S	SP28_primary_S	20	76962	62959184	0,5	-0,035923271	1	1	TRUE
SP28	primary_S	SP28_primary_S	21	9650104	48083526	0,5	-0,008482657	1	1	TRUE
SP28	primary_S	SP28_primary_S	22	16255826	51065831	0,5	-0,070960888	1	1	TRUE
SP28	primary_T	SP28_primary_T	1	808928	248813901	0,508	0,05366553	1	1	TRUE

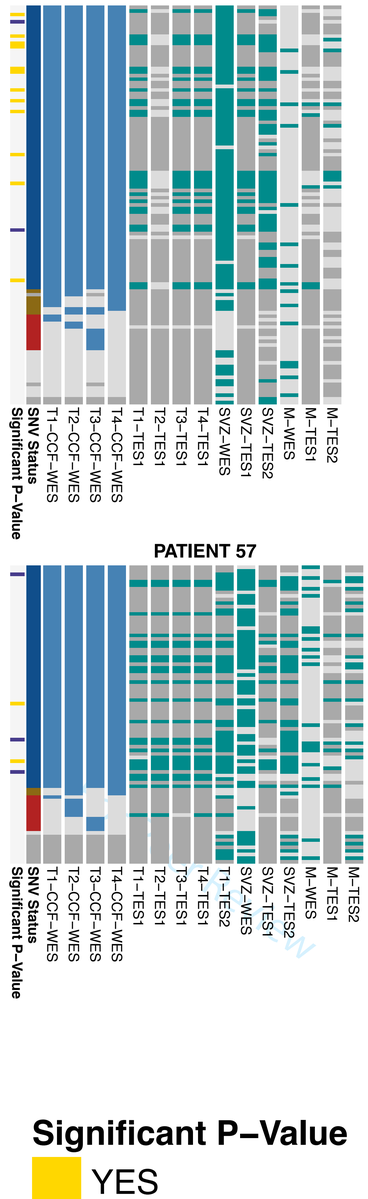
SP28	primary_T	SP28_primary_T	2	173150	242814463	0,582	-0,260783298	1	1	FALSE	
SP28	primary_T	SP28_primary_T	3	361508	197581147	0,536	0,029285458	1	1	FALSE	
SP28	primary_T	SP28_primary_T	4	60303	190905235	0,5	-0,15215363	1	1	TRUE	
SP28	primary_T	SP28_primary_T	5	163266	180670470	0,612	-0,12905774	1	1	FALSE	
SP28	primary_T	SP28_primary_T	6	335424	29855401	0,507	0,039995648	1	1	TRUE	
SP28	primary_T	SP28_primary_T	6	29855849	29855945	0,801	-0,584705214	1	0	FALSE	
SP28	primary_T	SP28_primary_T	6	29856330	29913483	0,514	0,005139506	1	1	TRUE	
SP28	primary_T	SP28_primary_T	6	29925456	29943067	0,722	0,07229471	2	1	TRUE	
SP28	primary_T	SP28_primary_T	6	29976789	31237727	0,505	0,014574939	1	1	TRUE	
SP28	primary_T	SP28_primary_T	6	31237767	31238372	0,73	0,06539921	2	1	FALSE	
SP28	primary_T	SP28_primary_T	6	31238490	32546696	0,557	-0,022170317	1	1	FALSE	
SP28	primary_T	SP28_primary_T	6	32546703	32546953	0,712	0,74820002	3	1	TRUE	
SP28	primary_T	SP28_primary_T	6	32548122	33085033	0,6	-0,015948396	1	1	FALSE	
SP28	primary_T	SP28_primary_T	6	33086249	170892848	0,5	0,021008012	1	1	TRUE	
SP28	primary_T	SP28_primary_T	7	296739	159024799	0,643	0,143697893	2	1	FALSE	
SP28	primary_T	SP28_primary_T	8	182949	146222122	0,506	0,099393536	1	1	TRUE	
SP28	primary_T	SP28_primary_T	9	154795	141070950	0,5	0,030283926	1	1	TRUE	
SP28	primary_T	SP28_primary_T	10	1052950	46143958	0,85	-0,405592404	1	0	FALSE	
SP28	primary_T	SP28_primary_T	10	46965018	47000146	0,605	-0,241240536	1	1	TRUE	
SP28	primary_T	SP28_primary_T	10	47605468	51549496	0,84	-0,338100277	1	0	FALSE	
SP28	primary_T	SP28_primary_T	10	51623061	51633027	0,538	-0,695305454	1	1	TRUE	
SP28	primary_T	SP28_primary_T	10	51785728	135279979	0,847	-0,398638533	1	0	FALSE	
SP28	primary_T	SP28_primary_T	11	193112	59860178	0,578	0,403108628	1	1	FALSE	

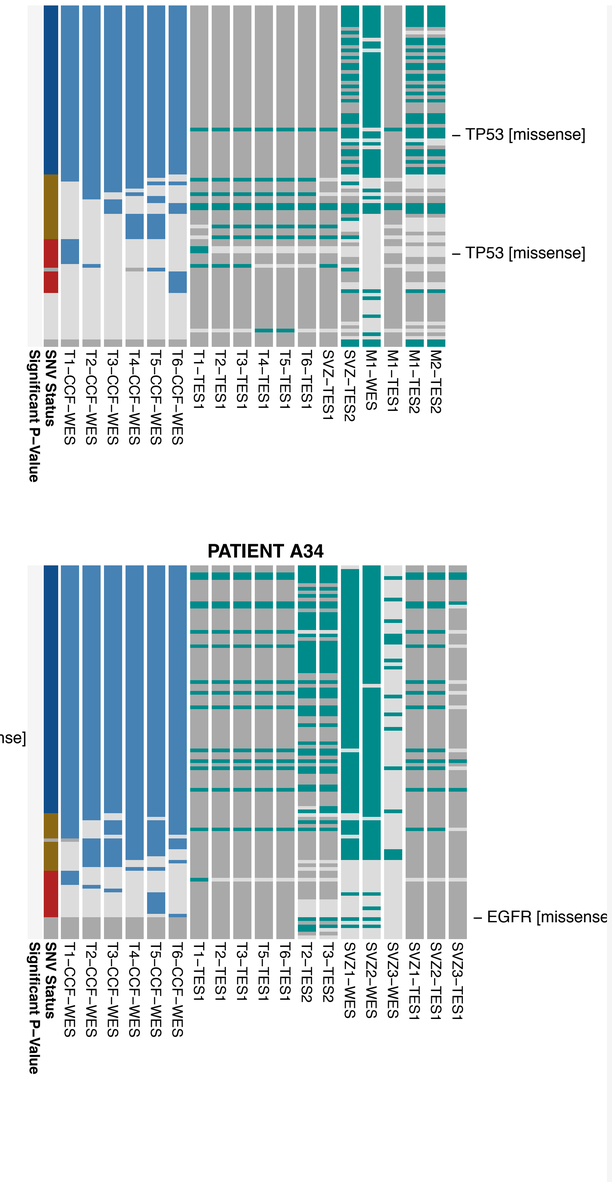
SP28	primary_T	SP28_primary_T	11	59940599	63072310	0,818	-0,541147973	1	0	FALSE			
SP28	primary_T	SP28_primary_T	11	63129782	64950970	0,5	0,060385147	1	1	TRUE			
SP28	primary_T	SP28_primary_T	11	64972354	70829858	0,81	-0,520963713	1	0	FALSE			
SP28	primary_T	SP28_primary_T	11	71260047	72316148	0,544	0,07686167	1	1	TRUE			
SP28	primary_T	SP28_primary_T	11	72407770	134856661	0,812	-0,549594238	1	0	FALSE			
SP28	primary_T	SP28_primary_T	12	310901	133808129	0,508	-0,134747941	1	1	TRUE			
SP28	primary_T	SP28_primary_T	13	19042581	42876290	0,5	0,143779013	1	1	TRUE			
SP28	primary_T	SP28_primary_T	13	43180503	95230412	0,836	-0,558197583	1	0	FALSE			
SP28	primary_T	SP28_primary_T	13	95275576	114323997	0,507	0,119452914	1	1	TRUE			
SP28	primary_T	SP28_primary_T	14	19411738	107283160	0,5	0,051310742	1	1	TRUE			
SP28	primary_T	SP28_primary_T	15	20169854	22788922	0,653	-0,557483034	1	0	FALSE			
SP28	primary_T	SP28_primary_T	15	22846965	102313869	0,81	-0,533854034	1	0	FALSE			
SP28	primary_T	SP28_primary_T	16	97610	90142087	0,5	-0,167248098	1	1	TRUE			
SP28	primary_T	SP28_primary_T	17	6115	2930339	0,891	0,235422346	2	0	FALSE			
SP28	primary_T	SP28_primary_T	17	2965929	2966308	0,529	-0,016470545	1	1	TRUE			
SP28	primary_T	SP28_primary_T	17	3144286	18252010	0,892	0,170198769	2	0	FALSE			
SP28	primary_T	SP28_primary_T	17	18314964	18380154	0,519	-0,459669711	1	1	TRUE			
SP28	primary_T	SP28_primary_T	17	18417838	21194785	0,876	0,221151974	2	0	FALSE			
SP28	primary_T	SP28_primary_T	17	21312542	81052423	0,5	0,186782701	1	1	TRUE			
SP28	primary_T	SP28_primary_T	18	196829	77896242	0,5	0,012921272	1	1	TRUE			
SP28	primary_T	SP28_primary_T	19	367089	7755285	0,719	0,422261851	2	1	FALSE			
SP28	primary_T	SP28_primary_T	19	7755482	7761667	0,948759057	0,246842257	2	0	TRUE			
SP28	primary_T	SP28_primary_T	19	7794609	59010819	0,709	0,412590001	2	1	FALSE			

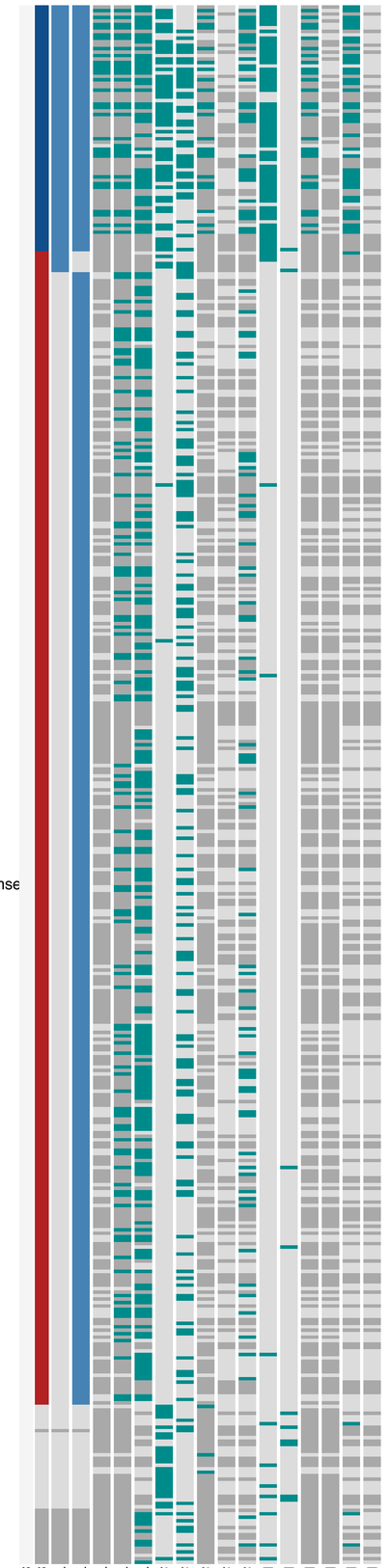
SP28	primary_T1	SP28_primary_T1	20	76962	58645262	0,625	-0,270698237
SP28	primary_T1	SP28_primary_T1	20	59829847	62959184	0,5	-0,068914521
SP28	primary_T1	SP28_primary_T1	21	9650104	11186346	0,5635	0,068148661
SP28	primary_T1	SP28_primary_T1	21	14433284	48083526	0,507	0,212492584
SP28	primary_T1	SP28_primary_T1	22	16255826	24622648	0,583	-0,040471716
SP28	primary_T1	SP28_primary_T1	22	24717518	51065831	0,5	0,173599111


PATIENT 42
SNV Status
Significant P–Value
T1–CCF–WES
T2–CCF–WES
T3–CCF–WES
T4–CCF–WES
T1–TES1
T2–TES1
T3–TES1
T4–TES1
SVZ–WES
SVZ–TES1
SVZ–TES2
M–WES
M–TES1
M–TES2


PATIENT 49
– TP53 [missense]
– LZTR1 [missense]
SNV Status
Significant P–Value
T1–CCF–WES
T2–CCF–WES
T3–CCF–WES
T4–CCF–WES
T1–TES1
T2–TES1
T3–TES1
T4–TES1
SVZ–WES
SVZ–TES1
SVZ–TES2
M–WES
M–TES1
M–TES2


PATIENT 52
SNV Status
Significant P–Value
T1–CCF–WES
T2–CCF–WES
T3–CCF–WES
T4–CCF–WES
T1–TES1
T2–TES1
T3–TES1
T4–TES1
SVZ–WES
SVZ–TES1
SVZ–TES2
M–WES
M–TES1
M–TES2


PATIENT 54
– TP53 [missense]
– TP53 [missense]
SNV Status
Significant P–Value
T1–CCF–WES
T2–CCF–WES
T3–CCF–WES
T4–CCF–WES
T5–CCF–WES
T6–CCF–WES
T1–TES1
T2–TES1
T3–TES1
T4–TES1
T5–TES1
T6–TES1
SVZ–TES1
SVZ–TES2
M1–WES
M1–TES1
M1–TES2
M2–TES2


PATIENT A23
SNV Status
Significant P–Value
T primary–CCF–WES
T recurrent–CCF–WES
T primary–TES1
T recurrent–TES1
T recurrent–TES2
SVZ primary–WES
SVZ primary–TES1
SVZ primary–TES2
SVZ recurrent–TES2
SVZ recurrent–WES
SVZ recurrent–TES1
M primary–WES
M recurrent–WES
M primary–TES1
M recurrent–TES1
M primary–TES2
M recurrent–TES2

PATIENT 55
– EGFR [missense]
– PIK3R1 [missense]
SNV Status
Significant P–Value
T1–CCF–WES
T2–CCF–WES
T3–CCF–WES
T4–CCF–WES
T2–TES1
T3–TES1
T4–TES1
T1–TES1
SVZ–WES
SVZ–TES1
SVZ–TES2
M–TES1

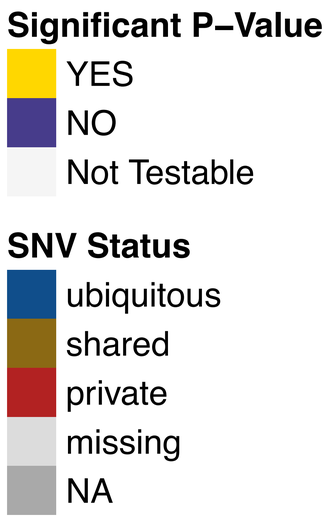
PATIENT 56
– PIK3R1 [missense]
– EGFR [missense]
SNV Status
Significant P–Value
T1–CCF–WES
T2–CCF–WES
T3–CCF–WES
T4–CCF–WES
T1–TES1
T2–TES1
T3–TES1
T4–TES1
T2–TES2
SVZ–WES
SVZ–TES1
SVZ–TES2
M–WES
M–TES1
M–TES2

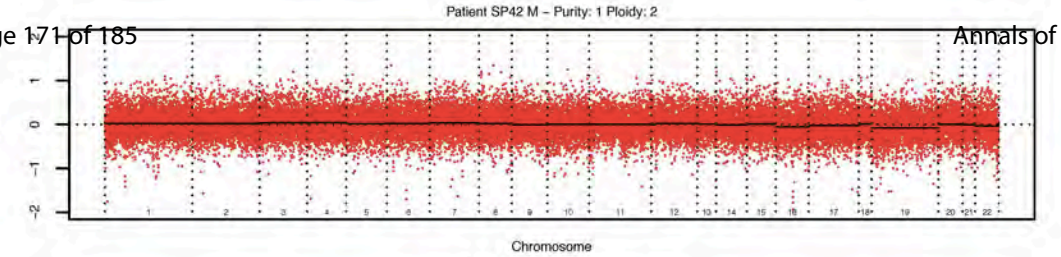
PATIENT 57
NE1 [stop]
NF1 [missense]
SNV Status
Significant P–Value
T1–CCF–WES
T2–CCF–WES
T3–CCF–WES
T4–CCF–WES
T1–TES1
T2–TES1
T3–TES1
T4–TES1
T1–TES2
SVZ–WES
SVZ–TES1
SVZ–TES2
M–WES
M–TES1
M–TES2

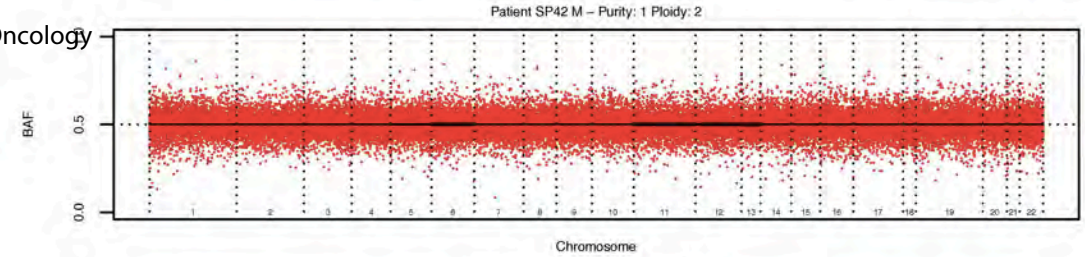
PATIENT A34
– EGFR [missense]
SNV Status
Significant P–Value
T1–CCF–WES
T2–CCF–WES
T3–CCF–WES
T4–CCF–WES
T5–CCF–WES
T6–CCF–WES
T1–TES1
T2–TES1
T3–TES1
T5–TES1
T6–TES1
T2–TES2
T3–TES2
SVZ1–WES
SVZ2–WES
SVZ3–WES
SVZ1–TES1
SVZ2–TES1
SVZ3–TES1

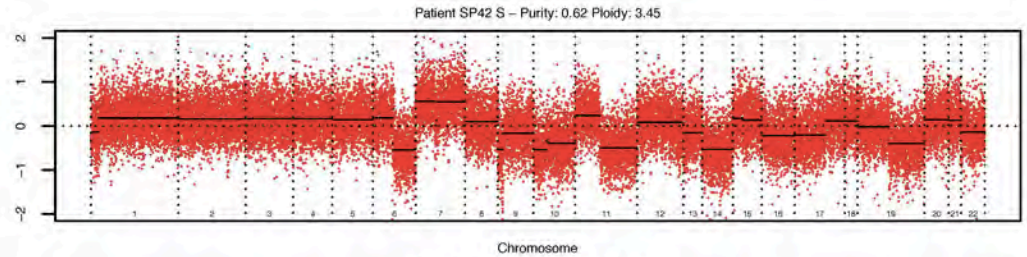
PATIENT A44
– PTEN [stop]
– EGFR [missense]
SNV Status
Significant P–Value
T1–CCF–WES
T2–CCF–WES
T3–CCF–WES
T5–CCF–WES
T1–TES1
T2–TES1
T3–TES1
T5–TES1
T2–TES2
T3–TES2
T5–TES2
SVZ–WES
SVZ–TES1
SVZ–TES2
M–WES
M–TES1
M–TES2

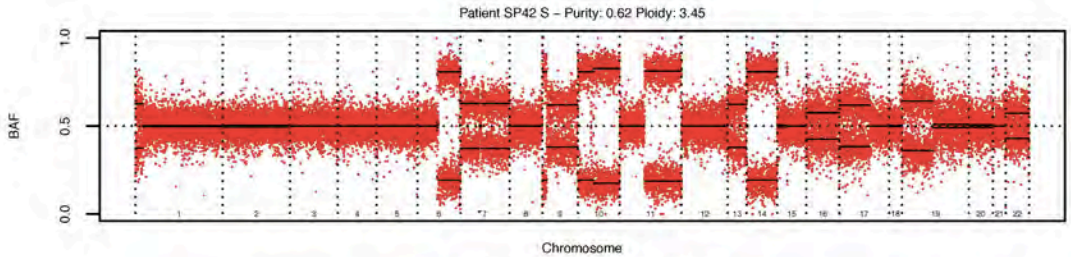
PATIENT SP28
– RB1 [stop]
– TP53 [missense]
SNV Status
Significant P–Value
T primary–CCF–WES
T recurrent–CCF–WES
T primary–TES1
T recurrent–TES1
SVZ primary–WES
SVZ recurrent–WES
SVZ primary–TES1
SVZ recurrent–TES1
SVZ primary–TES2
SVZ recurrent–TES2
M primary–WES
M recurrent–WES
M primary–TES1
M recurrent–TES1
M primary–TES2
M recurrent–TES2

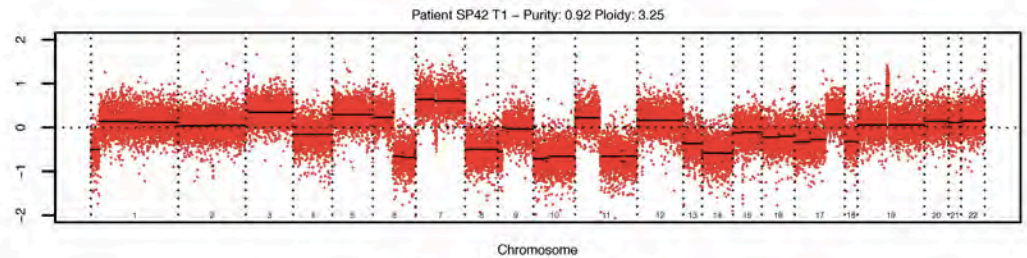

Significant P–Value
YES
NO
Not Testable
SNV Status
ubiquitous
shared
private
missing
NA

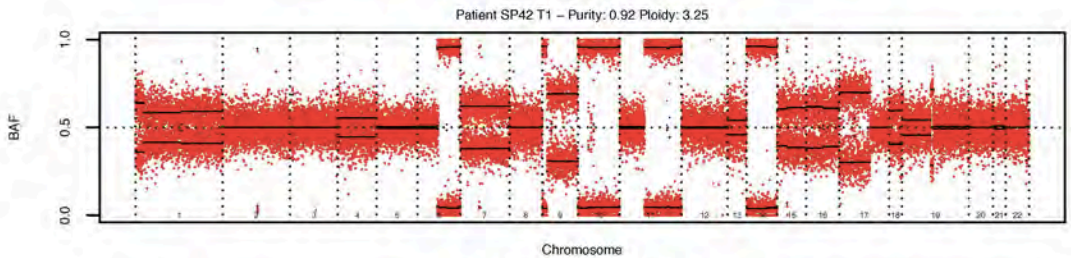

Patient SP42 M – Purity: 1 Ploidy: 2
LRR
Chromosome

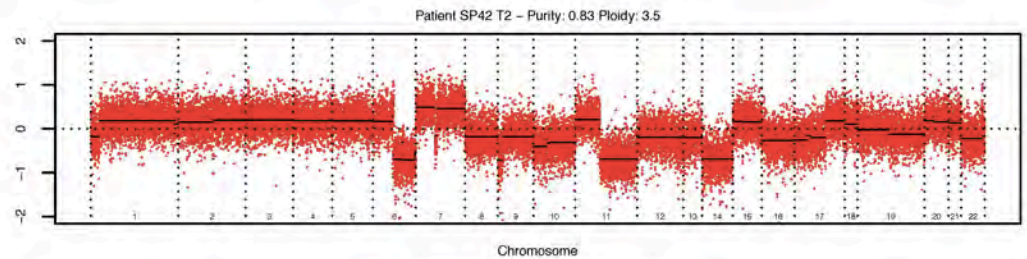

Patient SP42 M – Purity: 1 Ploidy: 2
BAF
Chromosome

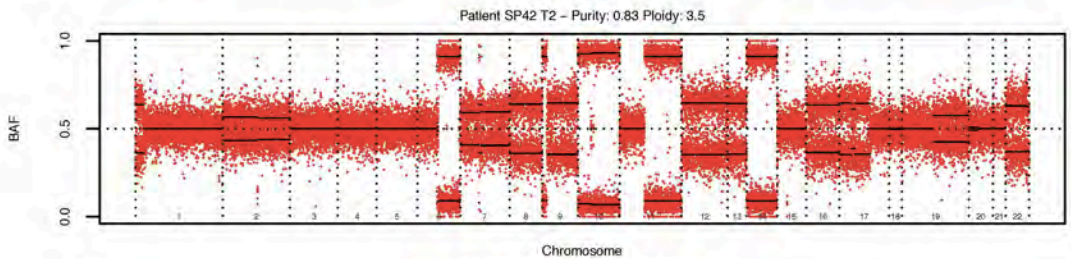

Patient SP42 S – Purity: 0.62 Ploidy: 3.45
LRR
Chromosome

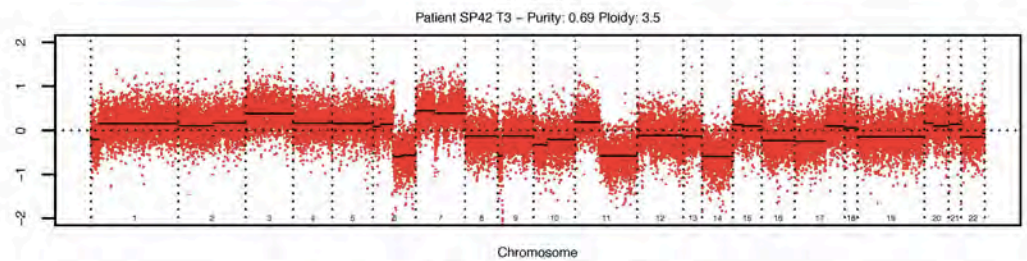

Patient SP42 S – Purity: 0.62 Ploidy: 3.45
BAF
Chromosome

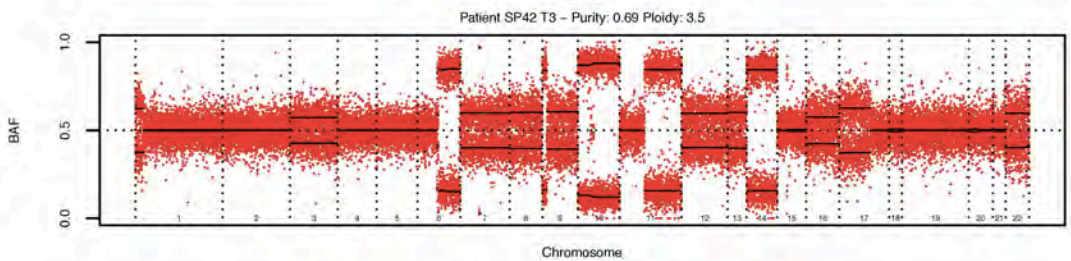

Patient SP42 T1 – Purity: 0.92 Ploidy: 3.25
LRR
Chromosome

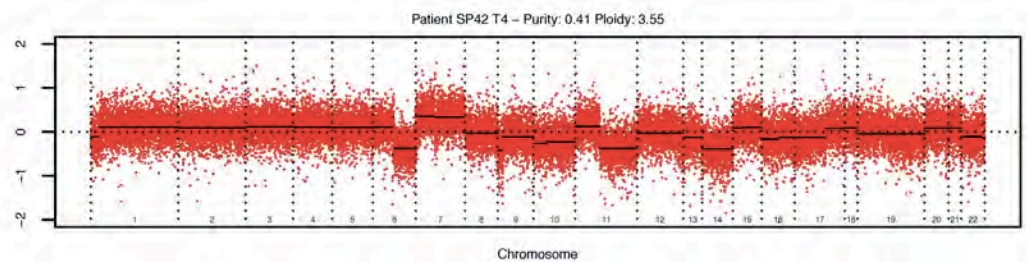

Patient SP42 T1 – Purity: 0.92 Ploidy: 3.25
BAF
Chromosome

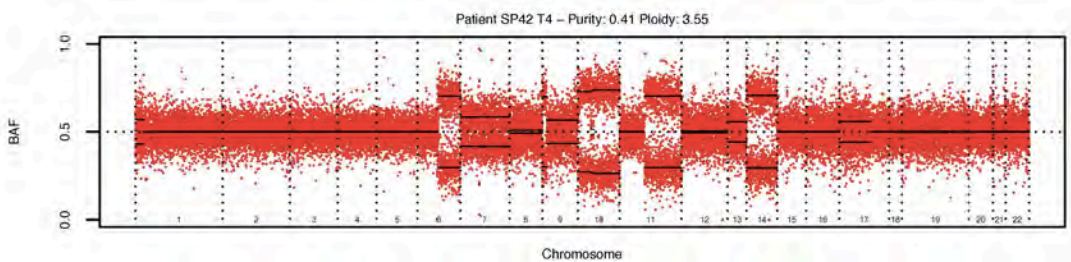

Patient SP42 T2 – Purity: 0.83 Ploidy: 3.5
LRR
Chromosome

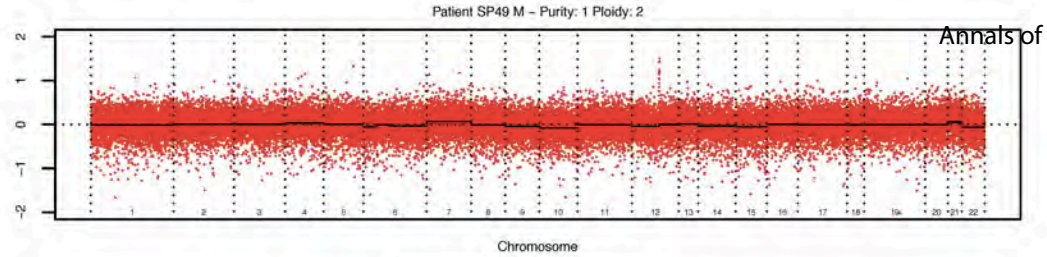

Patient SP42 T2 – Purity: 0.83 Ploidy: 3.5
BAF
Chromosome

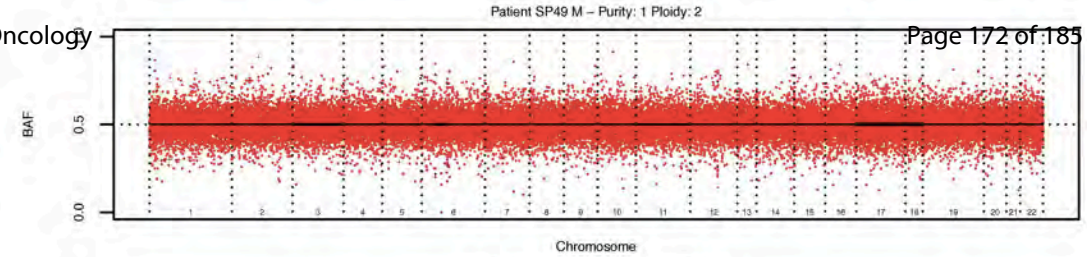

Patient SP42 T3 – Purity: 0.69 Ploidy: 3.5
LRR
Chromosome

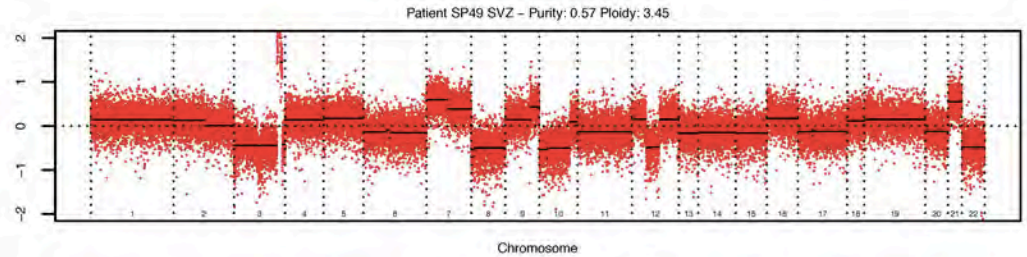

Patient SP42 T3 – Purity: 0.69 Ploidy: 3.5
BAF
Chromosome

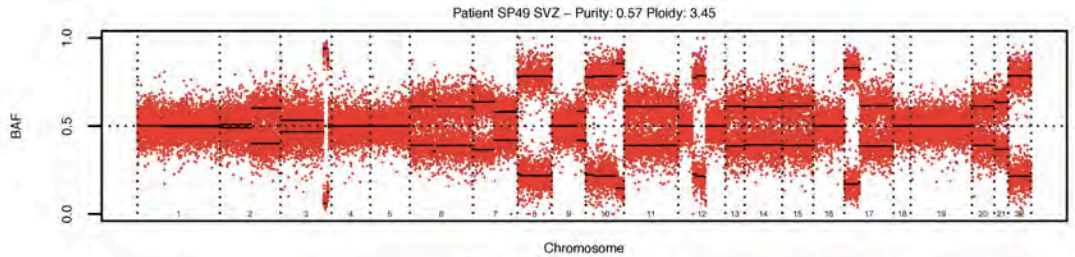

Patient SP42 T4 – Purity: 0.41 Ploidy: 3.55
LRR
Chromosome

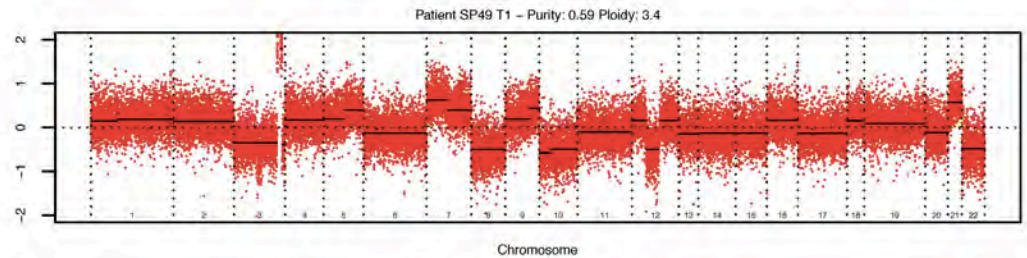

Patient SP42 T4 – Purity: 0.41 Ploidy: 3.55
BAF
Chromosome

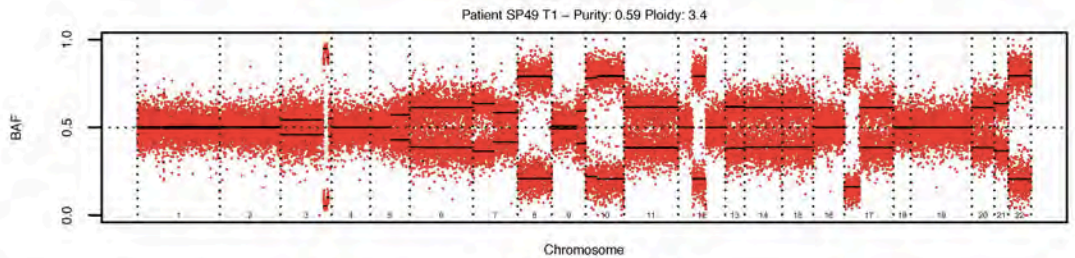

Patient SP49 M – Purity: 1 Ploidy: 2
LRR
Chromosome

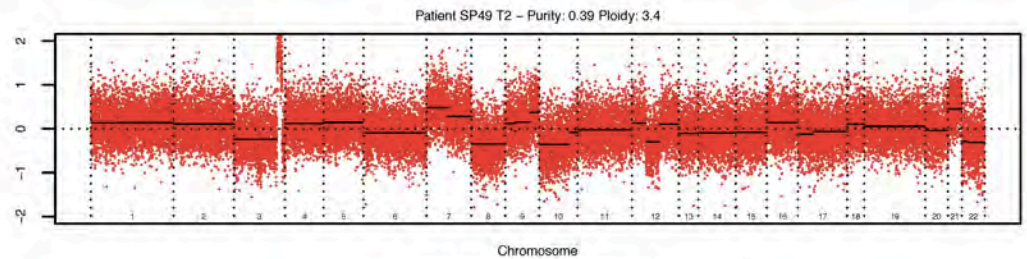

Patient SP49 M – Purity: 1 Ploidy: 2
BAF
Chromosome

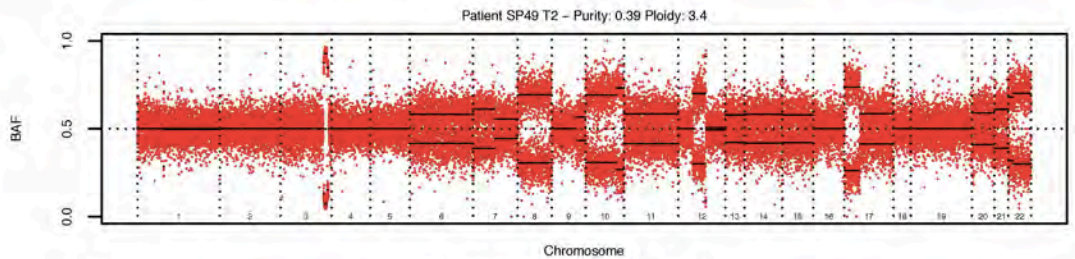

Patient SP49 SVZ – Purity: 0.57 Ploidy: 3.45
LRR
Chromosome

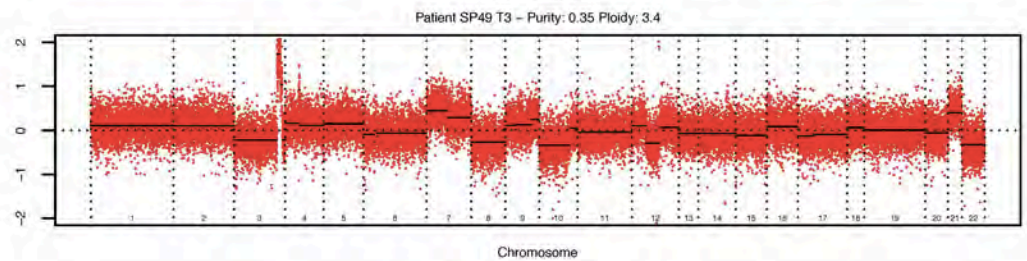

Patient SP49 SVZ – Purity: 0.57 Ploidy: 3.45
BAF
Chromosome

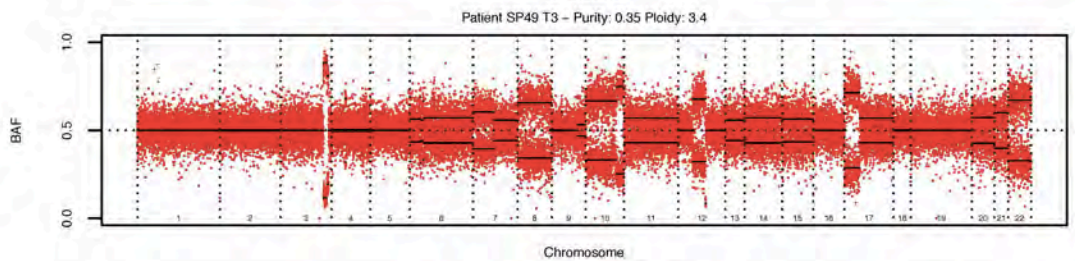

Patient SP49 T1 – Purity: 0.59 Ploidy: 3.4
LRR
Chromosome

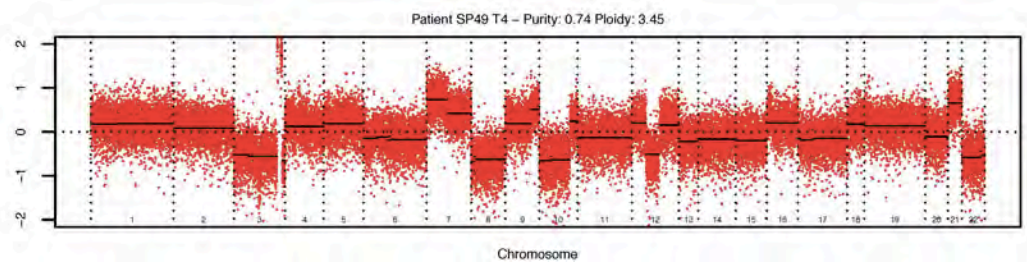

Patient SP49 T1 – Purity: 0.59 Ploidy: 3.4
BAF
Chromosome

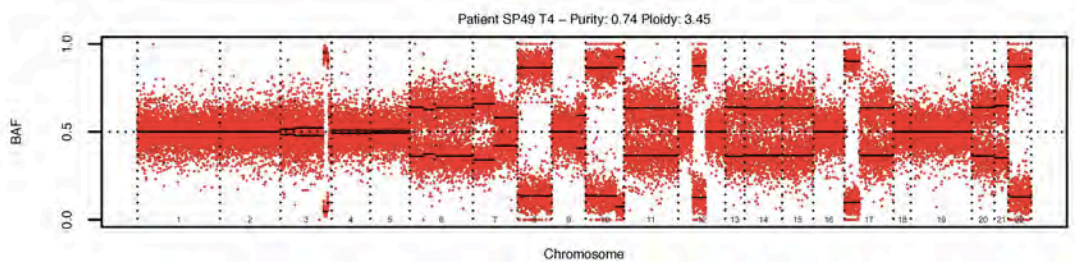

Patient SP49 T2 – Purity: 0.39 Ploidy: 3.4
LRR
Chromosome

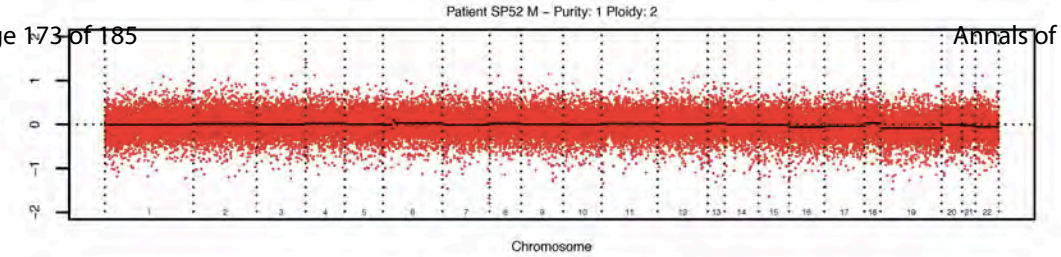

Patient SP49 T2 – Purity: 0.39 Ploidy: 3.4
BAF
Chromosome

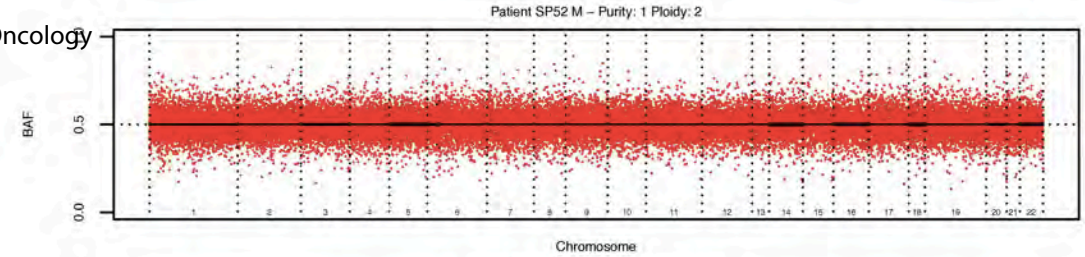

Patient SP49 T3 – Purity: 0.35 Ploidy: 3.4
LRR
Chromosome

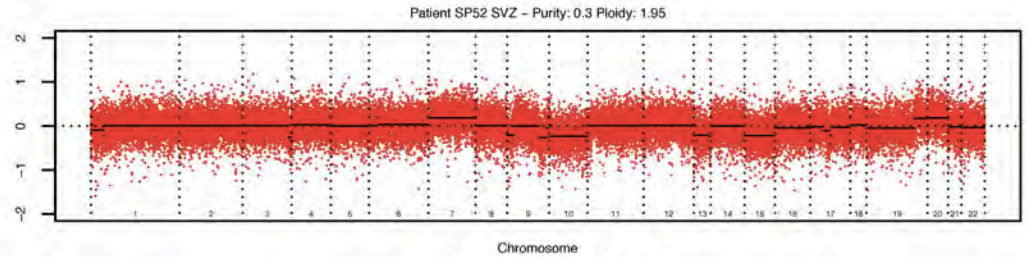

Patient SP49 T3 – Purity: 0.35 Ploidy: 3.4
BAF
Chromosome

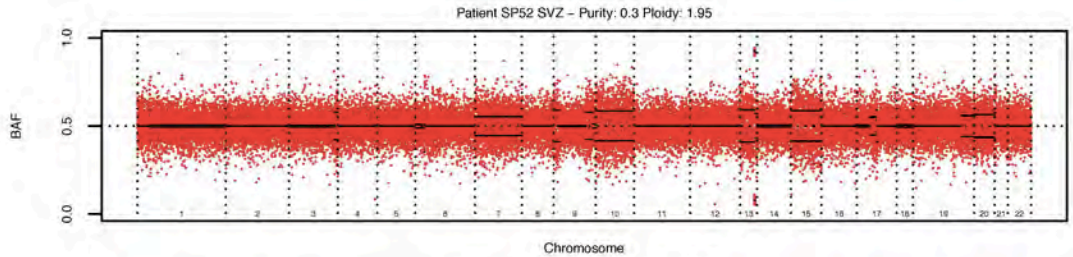

Patient SP49 T4 – Purity: 0.74 Ploidy: 3.45
LRR
Chromosome

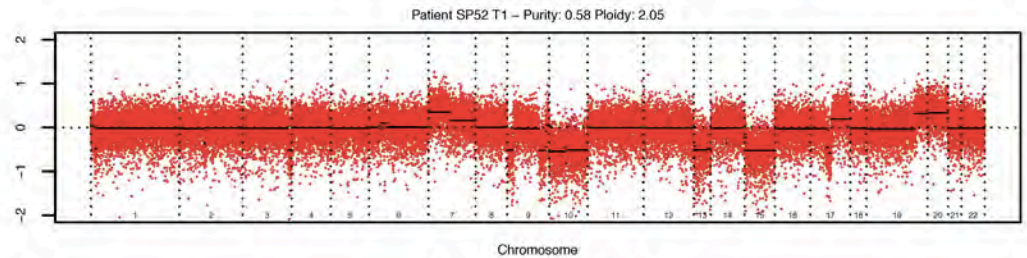

Patient SP49 T4 – Purity: 0.74 Ploidy: 3.45
BAF
Chromosome

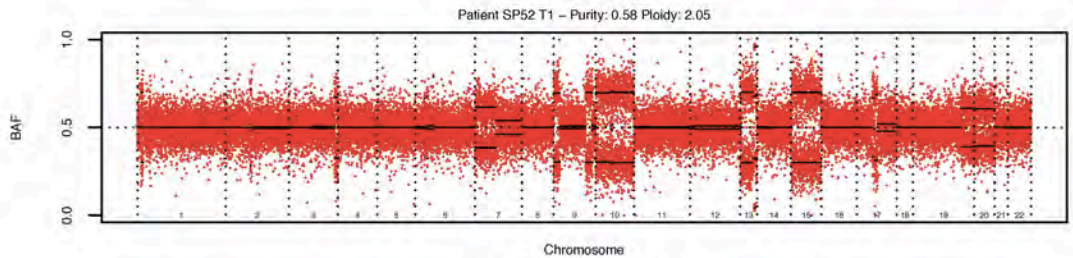

Patient SP52 M – Purity: 1 Ploidy: 2
LRR
Chromosome

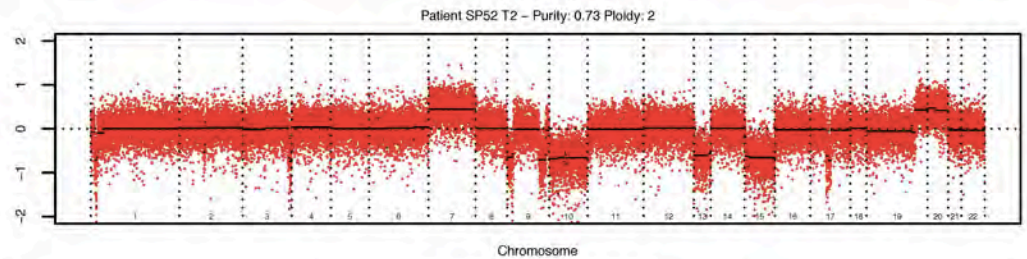

Patient SP52 M – Purity: 1 Ploidy: 2
BAF
Chromosome

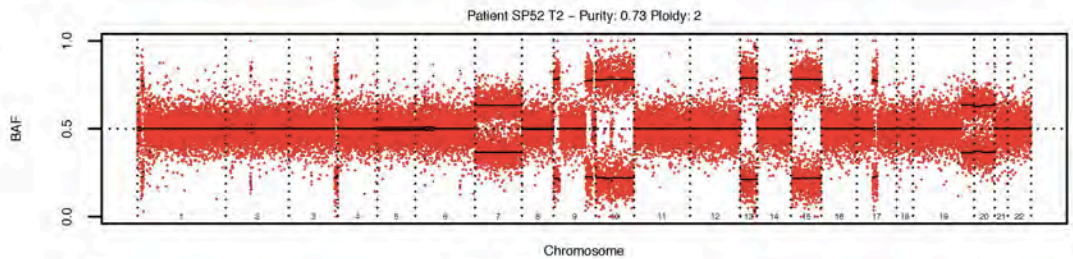

Patient SP52 SVZ – Purity: 0.3 Ploidy: 1.95
LRR
Chromosome

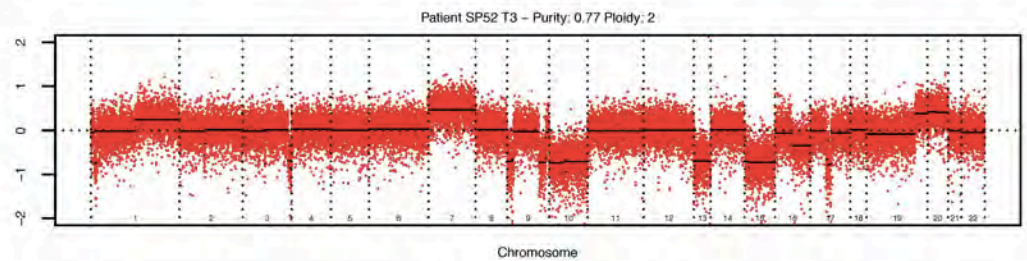

Patient SP52 SVZ – Purity: 0.3 Ploidy: 1.95
BAF
Chromosome

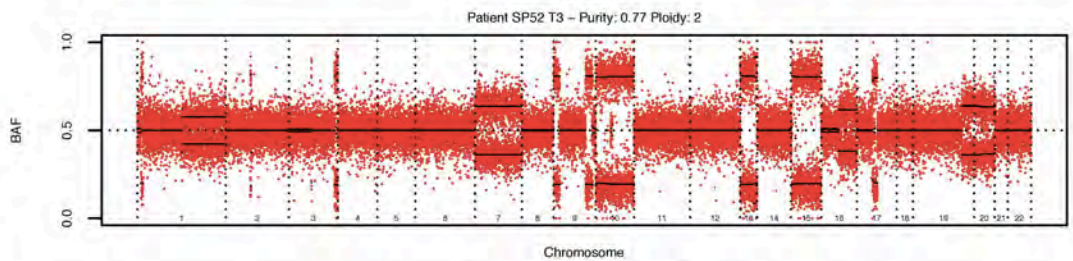

Patient SP52 T1 – Purity: 0.58 Ploidy: 2.05
LRR
Chromosome

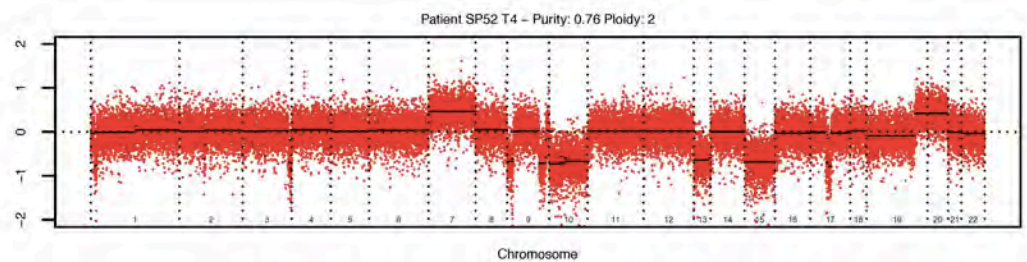

Patient SP52 T1 – Purity: 0.58 Ploidy: 2.05
BAF
Chromosome

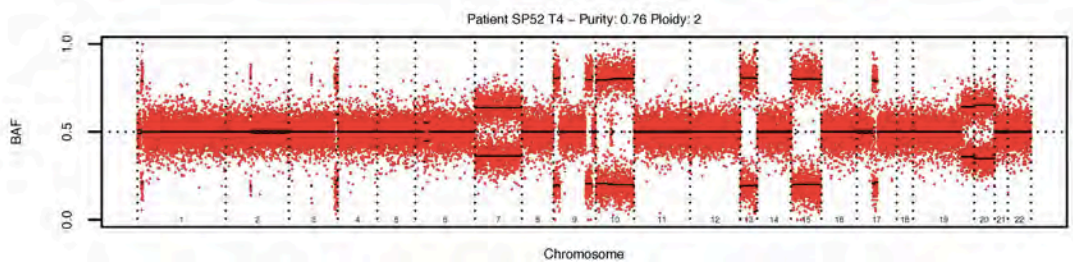

Patient SP52 T2 – Purity: 0.73 Ploidy: 2
LRR
Chromosome

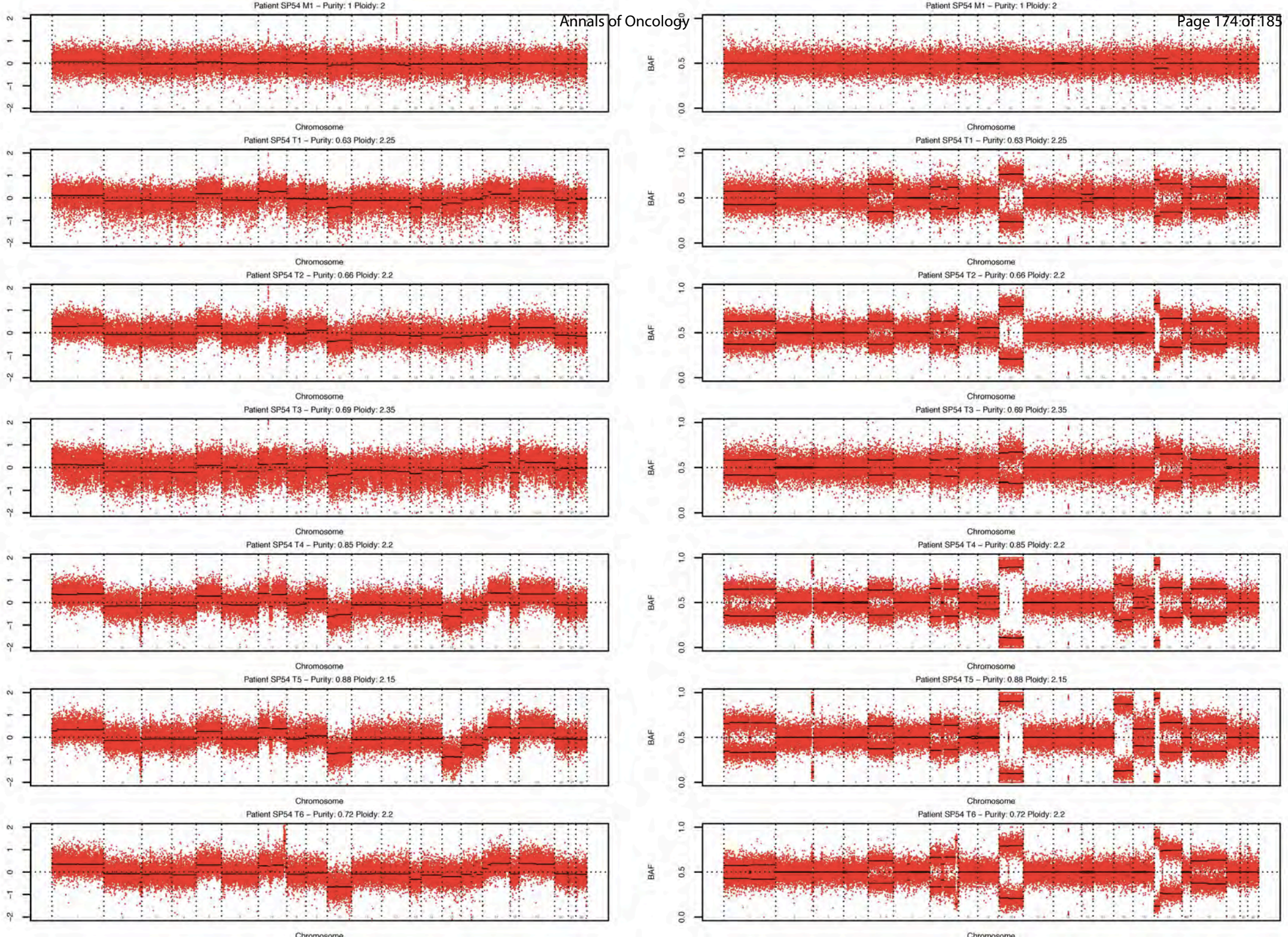

Patient SP52 T2 – Purity: 0.73 Ploidy: 2
BAF
Chromosome

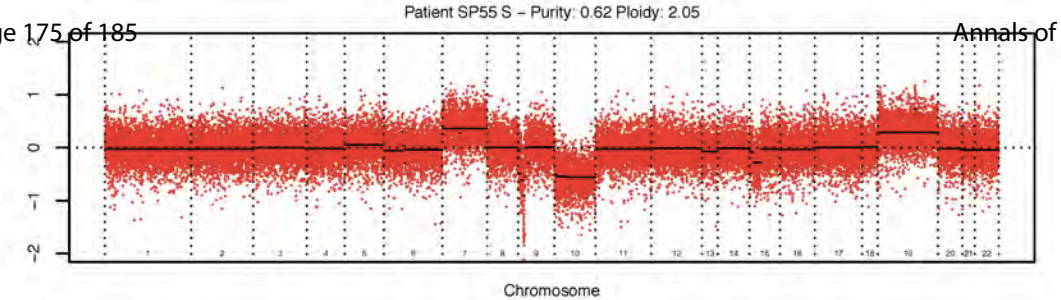

Patient SP52 T3 – Purity: 0.77 Ploidy: 2
LRR
Chromosome

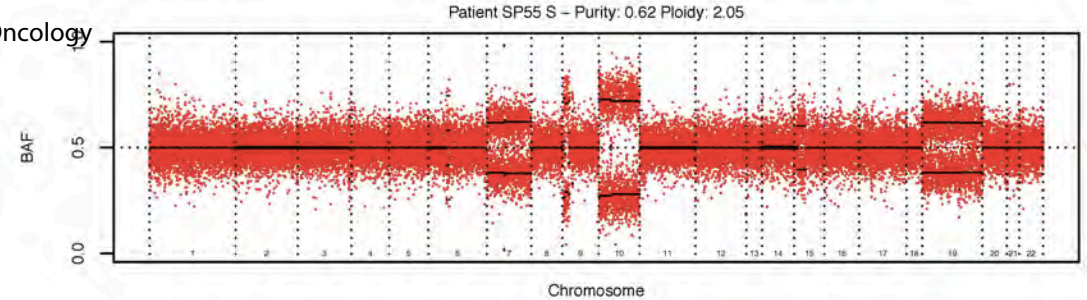

Patient SP52 T3 – Purity: 0.77 Ploidy: 2
BAF
Chromosome

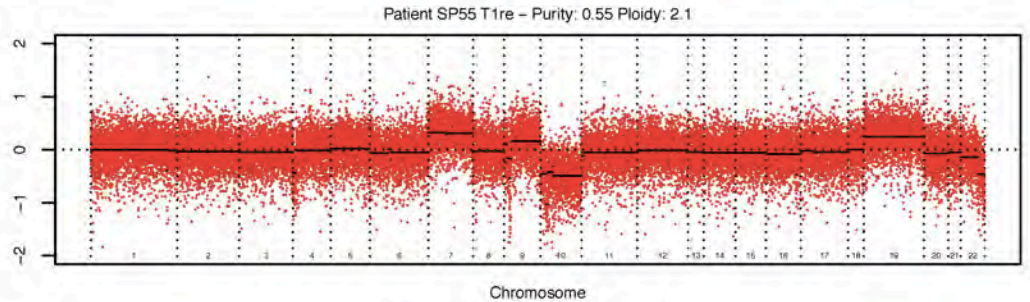

Patient SP52 T4 – Purity: 0.76 Ploidy: 2
LRR
Chromosome

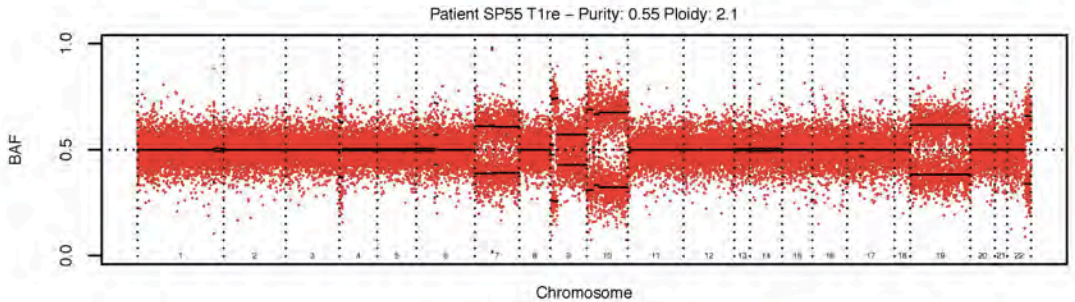

Patient SP52 T4 – Purity: 0.76 Ploidy: 2
BAF
Chromosome

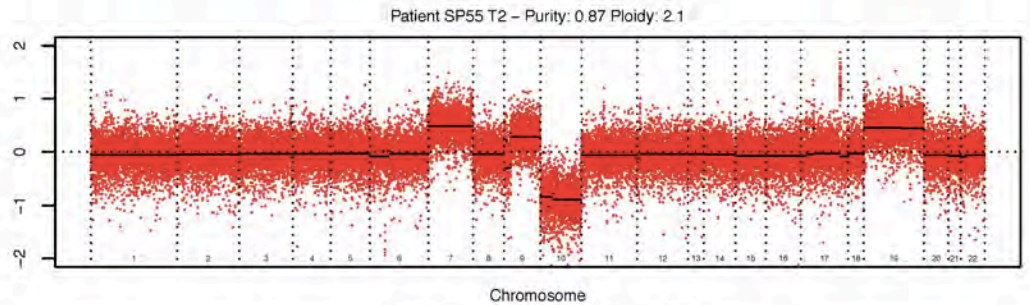

Patient SP54 M1 – Purity: 1 Ploidy: 2
Patient SP54 T1 – Purity: 0.63 Ploidy: 2.25
Patient SP54 T2 – Purity: 0.66 Ploidy: 2.2
Patient SP54 T3 – Purity: 0.69 Ploidy: 2.35
Patient SP54 T4 – Purity: 0.85 Ploidy: 2.2
Patient SP54 T5 – Purity: 0.88 Ploidy: 2.15
Patient SP54 T6 – Purity: 0.72 Ploidy: 2.2
LRR
BAF
Chromosome

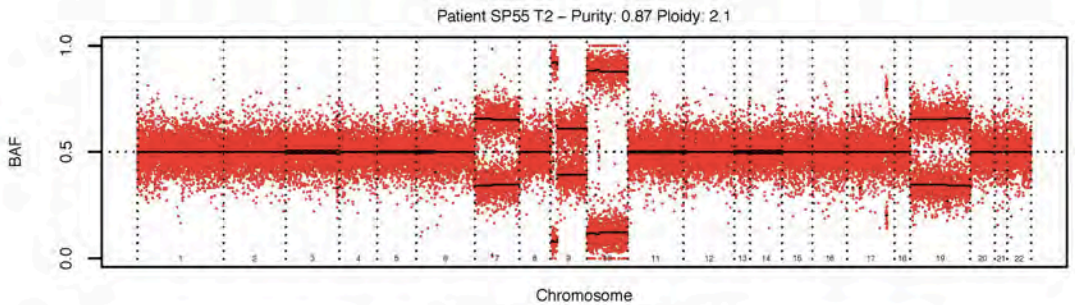

Patient SP55 S – Purity: 0.62 Ploidy: 2.05
LRR
Chromosome

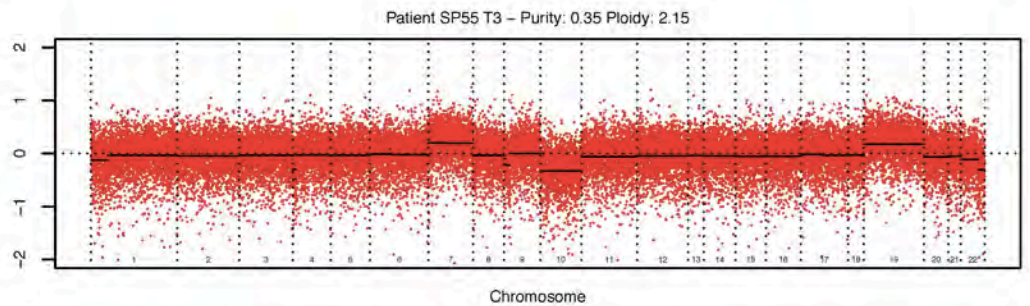

Patient SP55 S – Purity: 0.62 Ploidy: 2.05
BAF
Chromosome

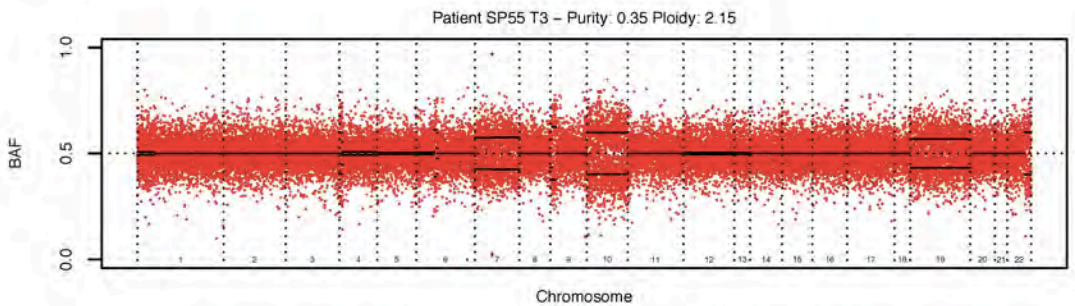

Patient SP55 T1re – Purity: 0.55 Ploidy: 2.1
LRR
Chromosome

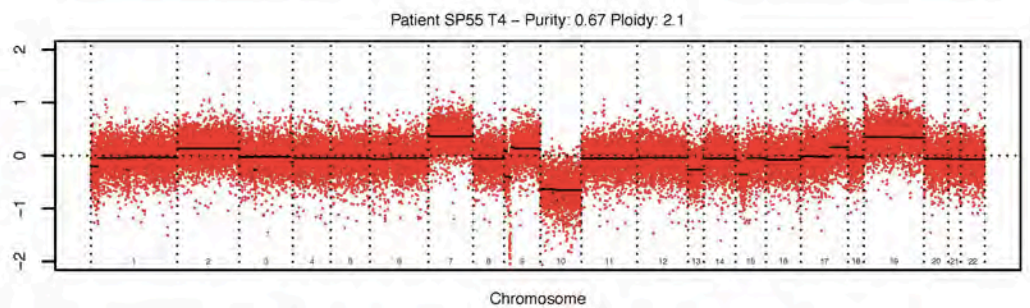

Patient SP55 T1re – Purity: 0.55 Ploidy: 2.1
BAF
Chromosome

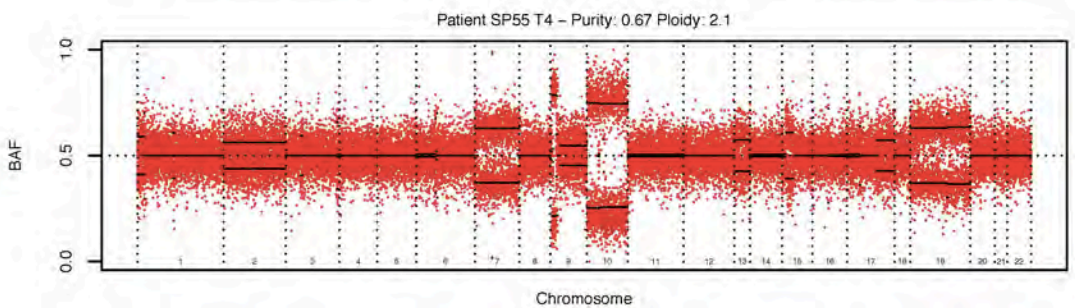

Patient SP55 T2 – Purity: 0.87 Ploidy: 2.1
LRR
Chromosome

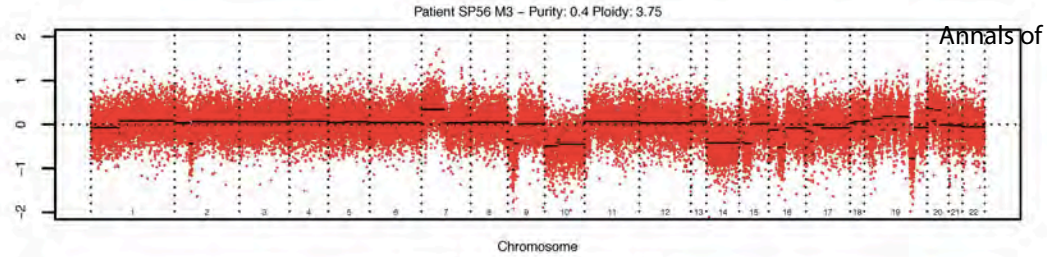

Patient SP55 T2 – Purity: 0.87 Ploidy: 2.1
BAF
Chromosome

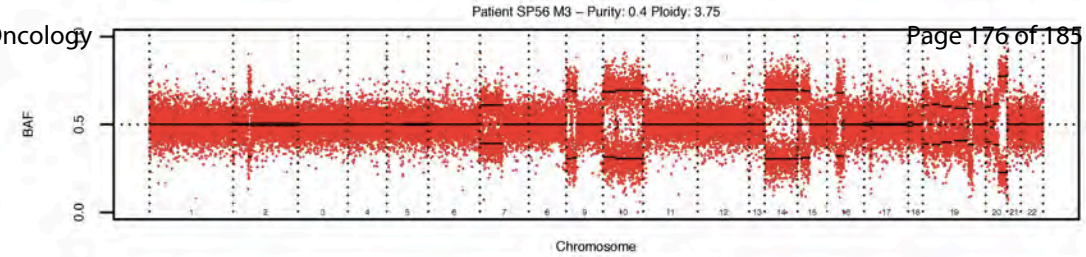

Patient SP55 T3 – Purity: 0.35 Ploidy: 2.15
LRR
Chromosome

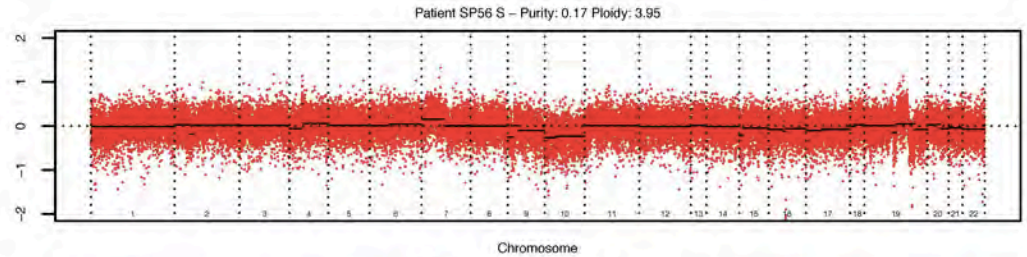

Patient SP55 T3 – Purity: 0.35 Ploidy: 2.15
BAF
Chromosome

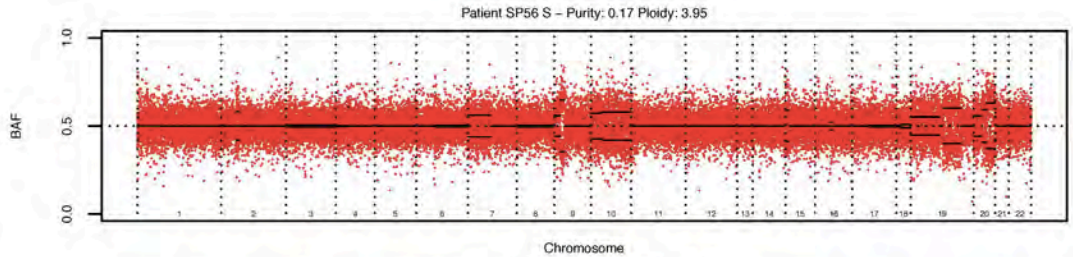

Patient SP55 T4 – Purity: 0.67 Ploidy: 2.1
LRR
Chromosome

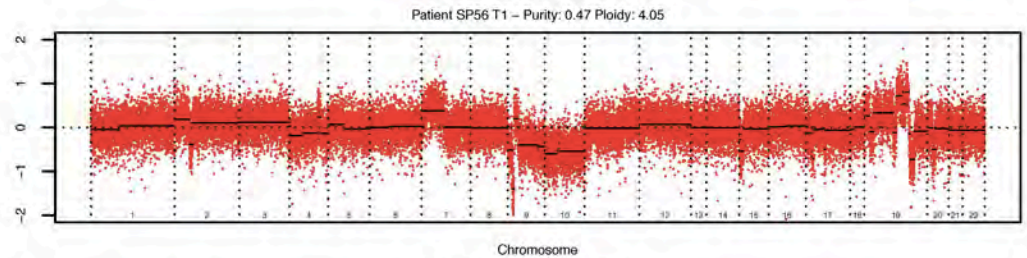

Patient SP55 T4 – Purity: 0.67 Ploidy: 2.1
BAF
Chromosome

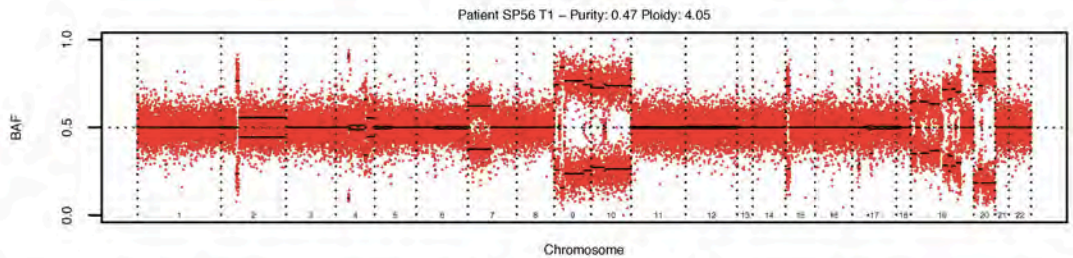

Patient SP56 M3 – Purity: 0.4 Ploidy: 3.75
LRR
Chromosome

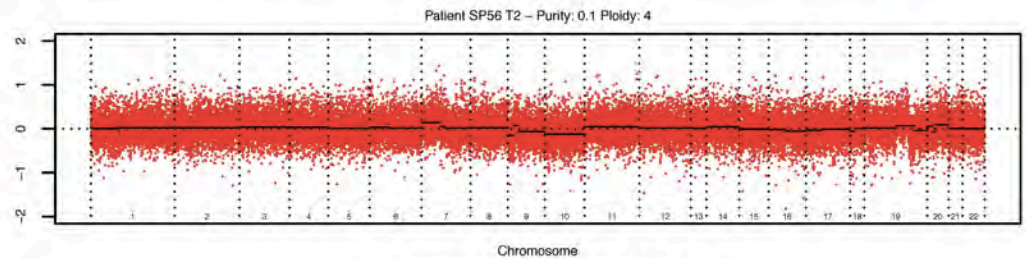

Patient SP56 M3 – Purity: 0.4 Ploidy: 3.75
BAF
Chromosome

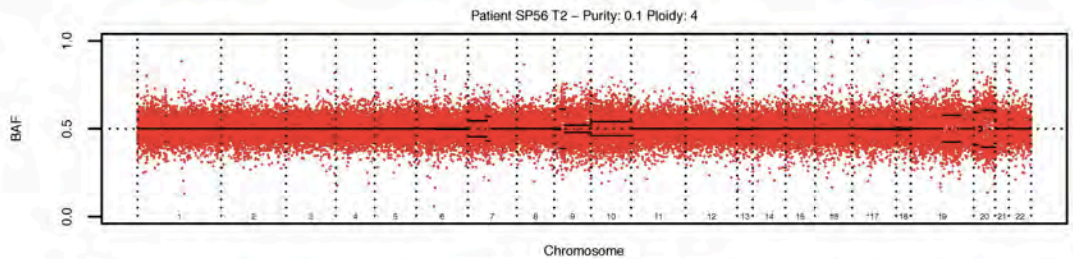

Patient SP56 S – Purity: 0.17 Ploidy: 3.95
LRR
Chromosome

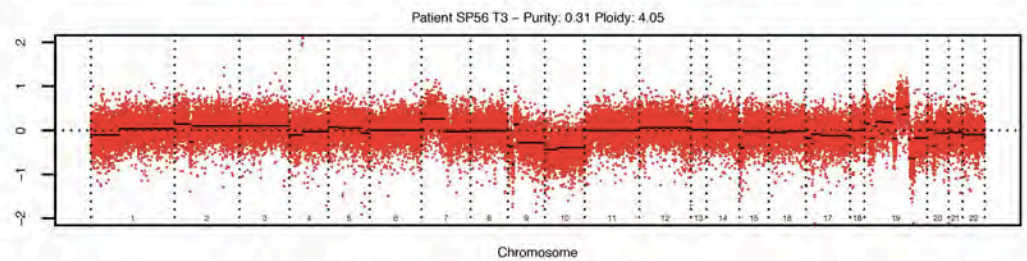

Patient SP56 S – Purity: 0.17 Ploidy: 3.95
BAF
Chromosome

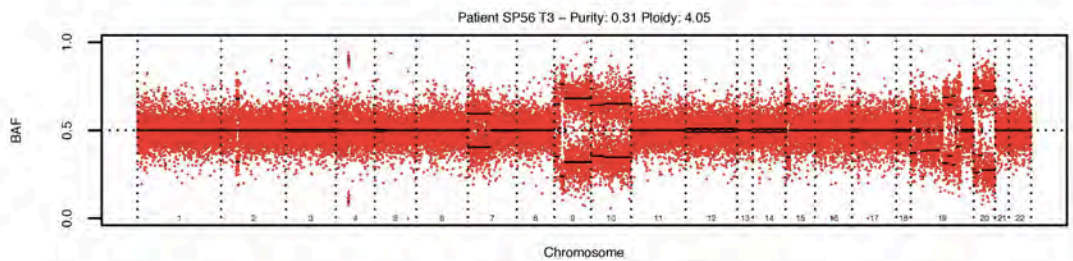

Patient SP56 T1 – Purity: 0.47 Ploidy: 4.05
LRR
Chromosome

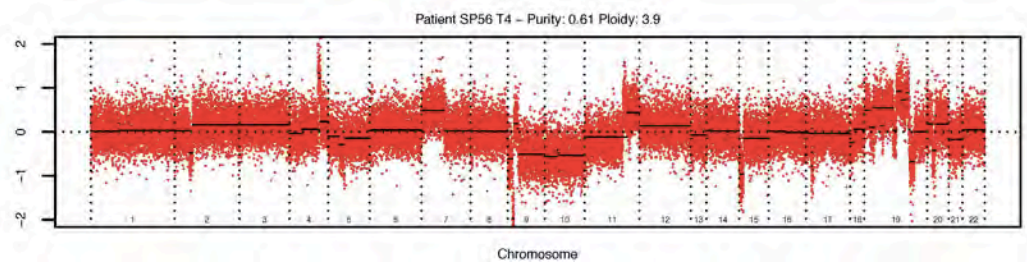

Patient SP56 T1 – Purity: 0.47 Ploidy: 4.05
BAF
Chromosome

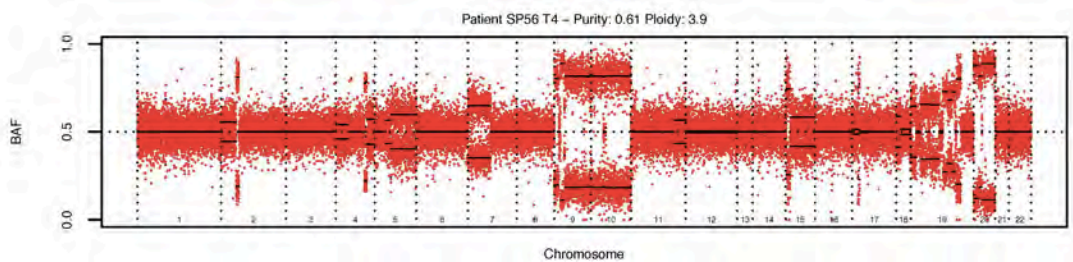

Patient SP56 T2 – Purity: 0.1 Ploidy: 4
LRR
Chromosome

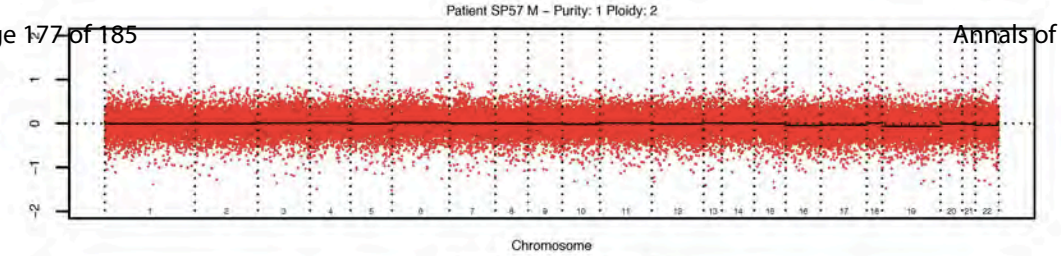

Patient SP56 T2 – Purity: 0.1 Ploidy: 4
BAF
Chromosome

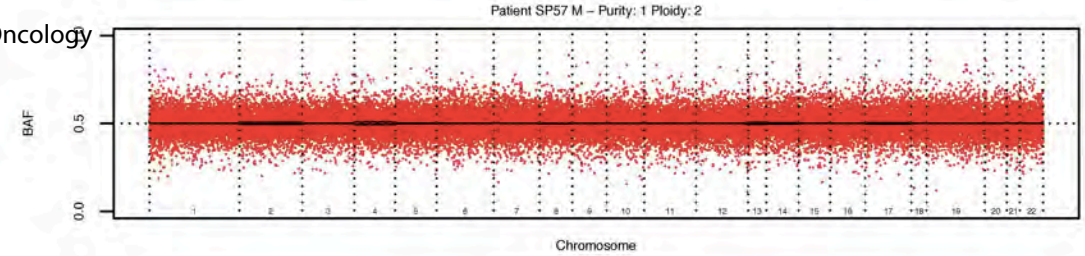

Patient SP56 T3 – Purity: 0.31 Ploidy: 4.05
LRR
Chromosome


Patient SP56 T3 – Purity: 0.31 Ploidy: 4.05
BAF
Chromosome


Patient SP56 T4 – Purity: 0.61 Ploidy: 3.9
LRR
Chromosome


Patient SP56 T4 – Purity: 0.61 Ploidy: 3.9
BAF
Chromosome


Patient SP57 M – Purity: 1 Ploidy: 2
LRR
Chromosome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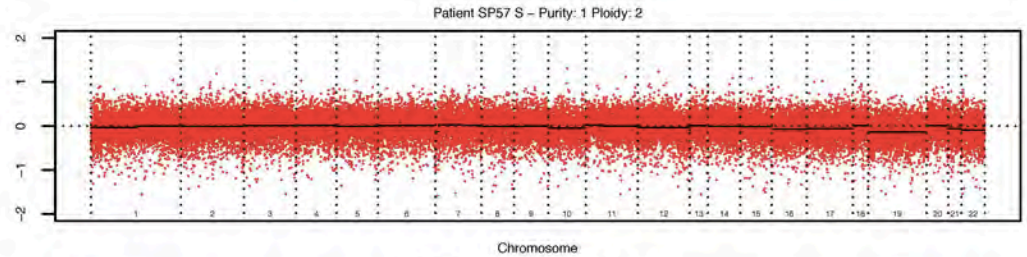
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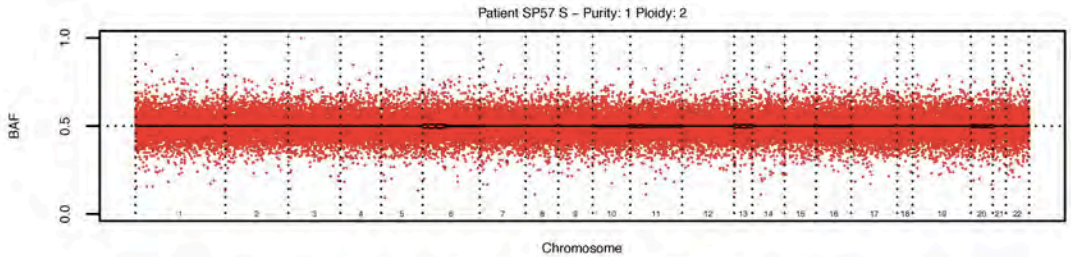
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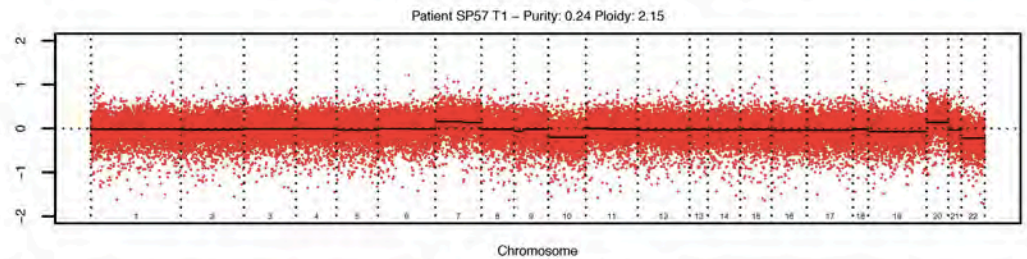
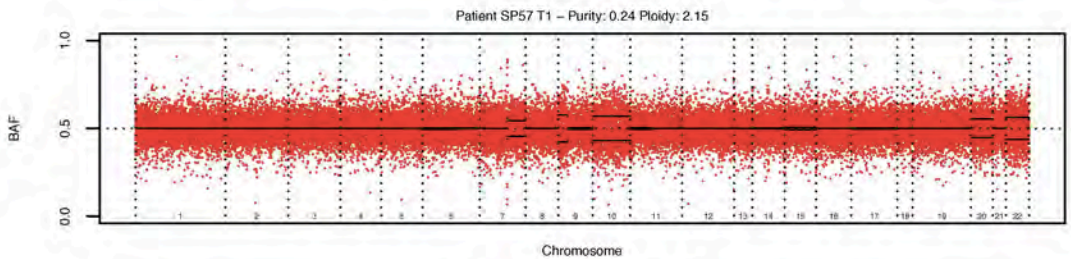
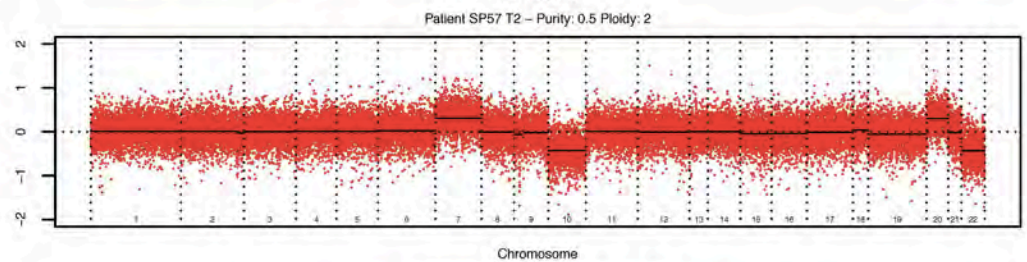
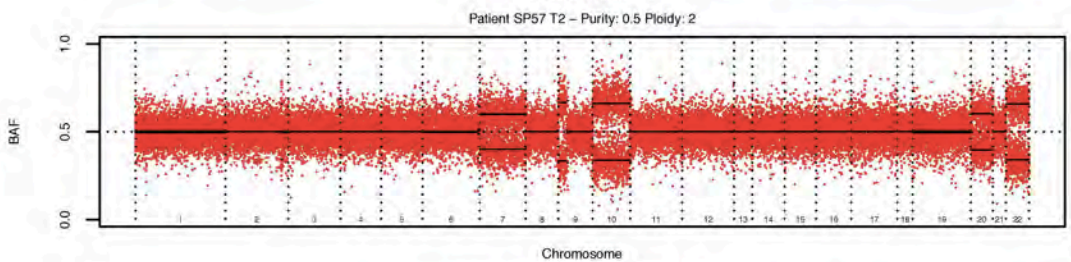
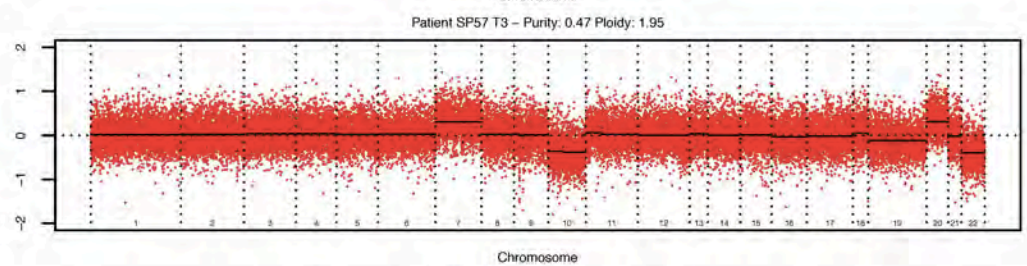
Chromosome

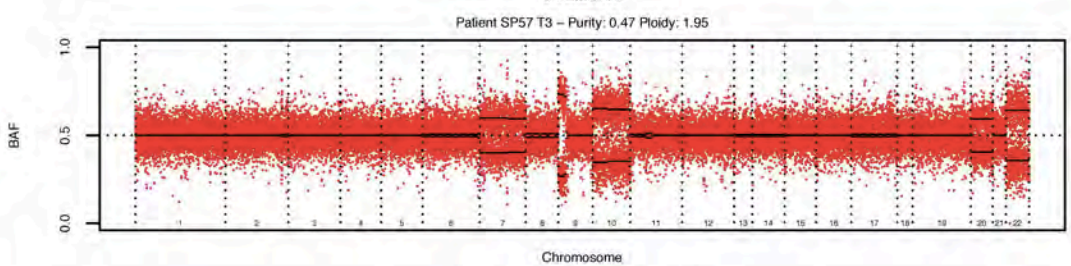

Patient SP57 T1 – Purity: 0.24 Ploidy: 2.15
LRR
Chromosome

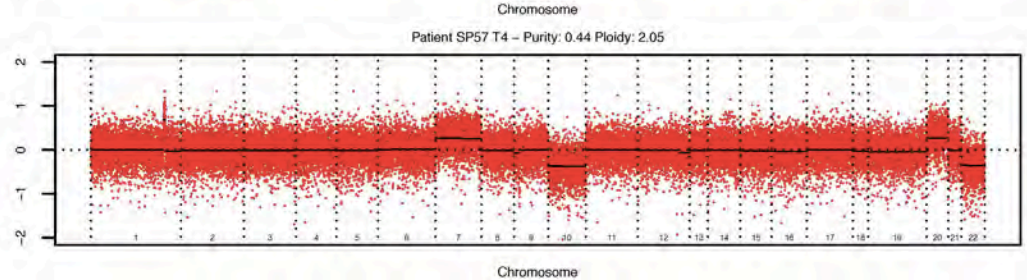

Patient SP57 T1 – Purity: 0.24 Ploidy: 2.15
BAF
Chromosome

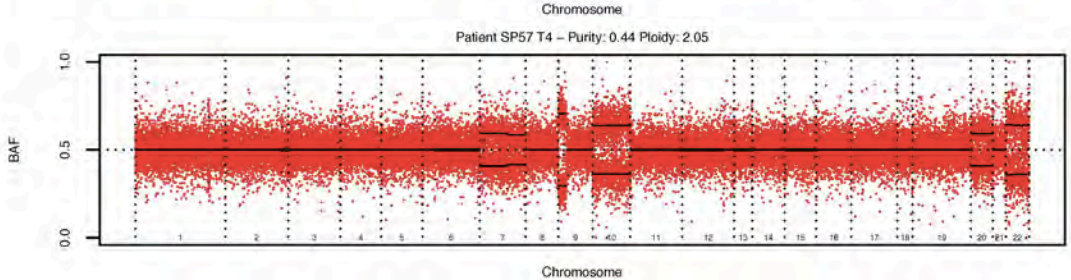

Patient SP57 T2 – Purity: 0.5 Ploidy: 2
LRR
Chromosome

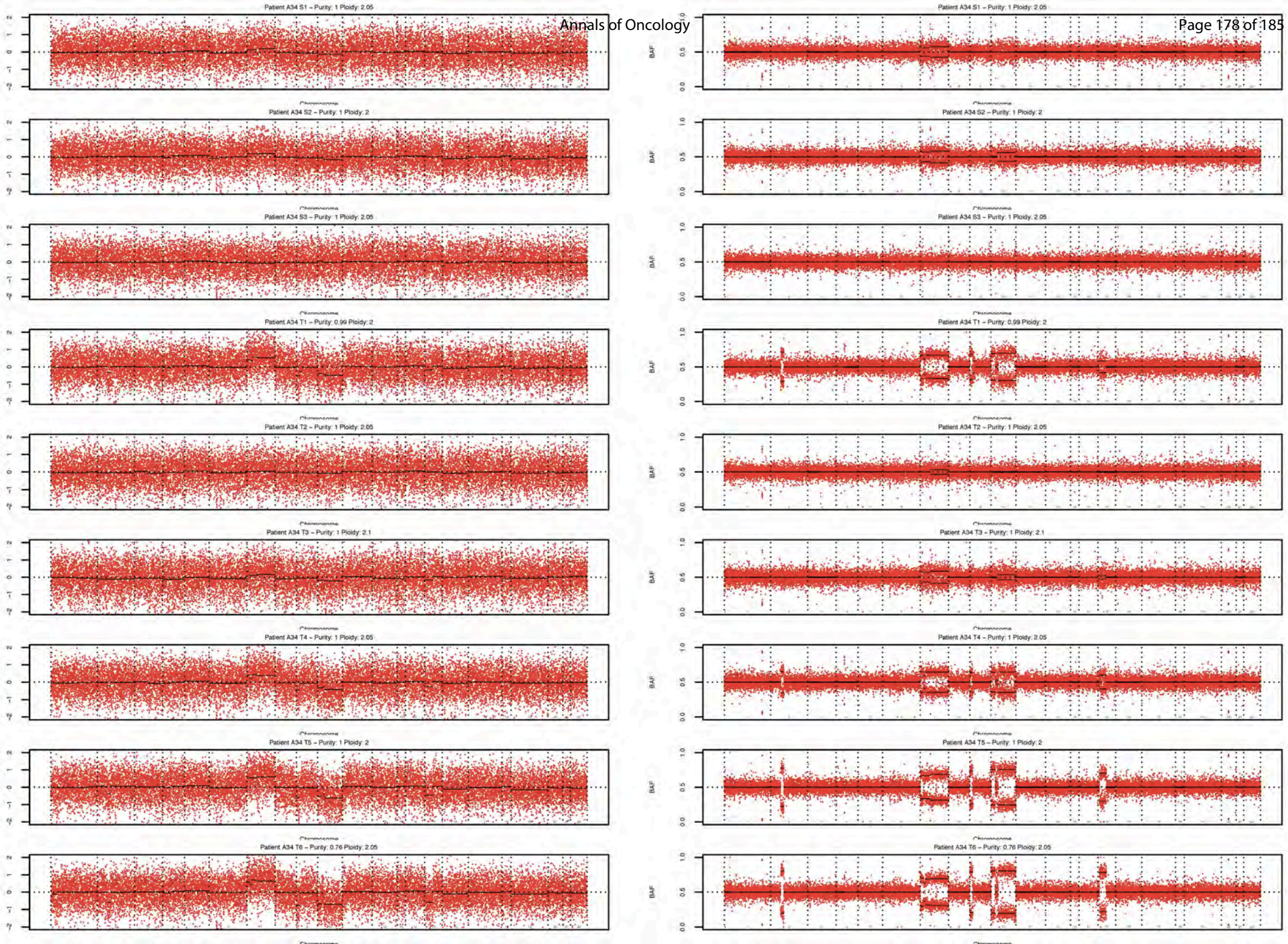

Patient SP57 T2 – Purity: 0.5 Ploidy: 2
BAF
Chromosome

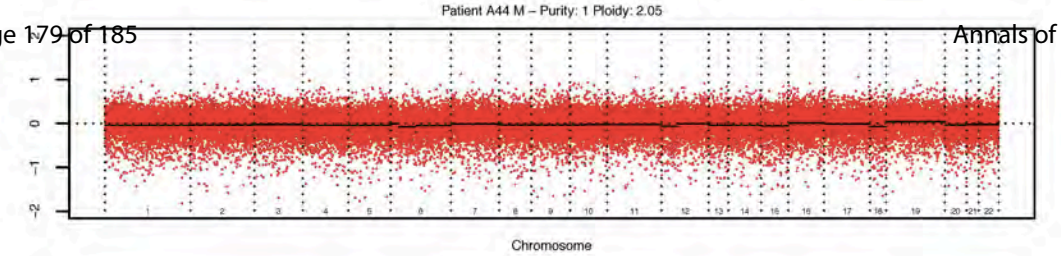

Patient SP57 T3 – Purity: 0.47 Ploidy: 1.95
LRR
Chromosome

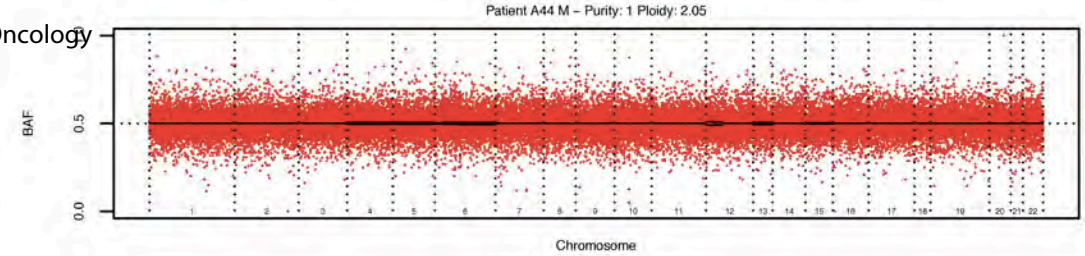

Patient SP57 T3 – Purity: 0.47 Ploidy: 1.95
BAF
Chromosome

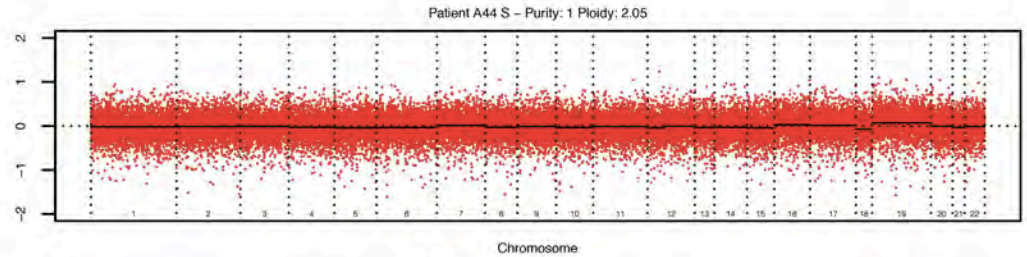

Patient SP57 T4 – Purity: 0.44 Ploidy: 2.05
LRR
Chromosome

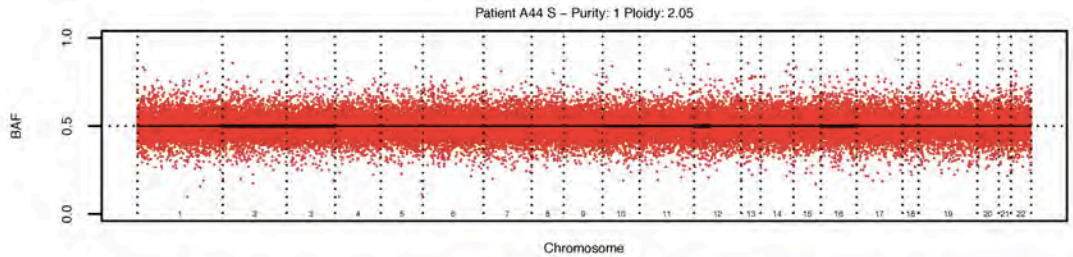

Patient SP57 T4 – Purity: 0.44 Ploidy: 2.05
BAF
Chromosome

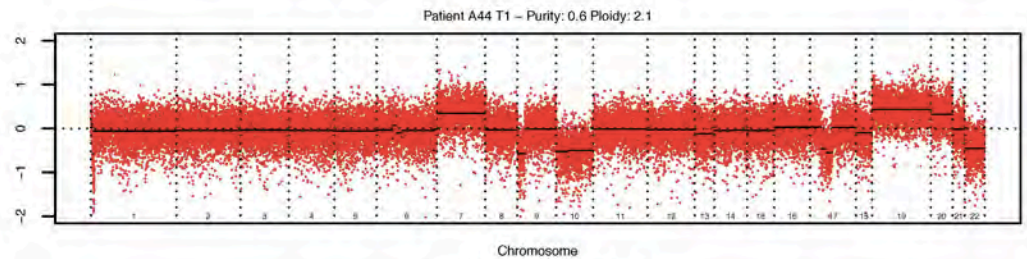

Patient A34 S1 – Purity: 1 Ploidy: 2.05
Patient A34 S2 – Purity: 1 Ploidy: 2
Patient A34 S3 – Purity: 1 Ploidy: 2.05
Patient A34 T1 – Purity: 0.99 Ploidy: 2
Patient A34 T2 – Purity: 1 Ploidy: 2.05
Patient A34 T3 – Purity: 1 Ploidy: 2.1
Patient A34 T4 – Purity: 1 Ploidy: 2.05
Patient A34 T5 – Purity: 1 Ploidy: 2
Patient A34 T6 – Purity: 0.76 Ploidy: 2.05
LRR
BAF
Chromosome

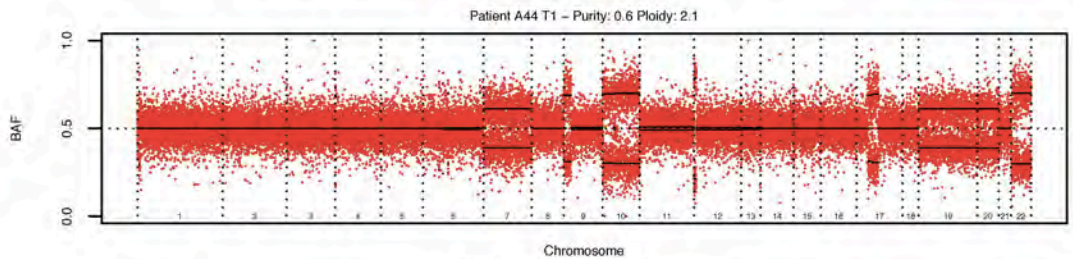

Patient A44 M – Purity: 1 Ploidy: 2.05
LRR
Chromosome

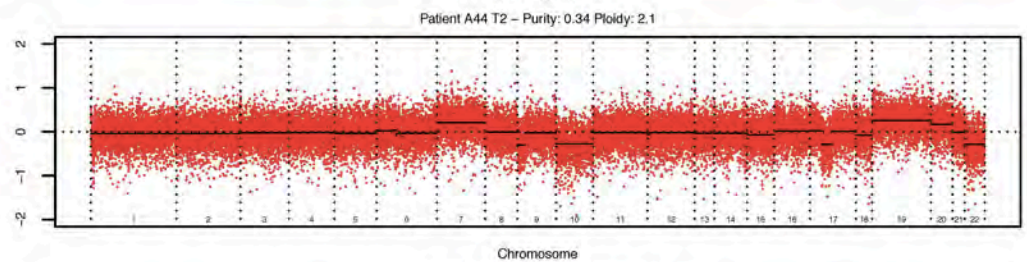

Patient A44 M – Purity: 1 Ploidy: 2.05
BAF
Chromosome

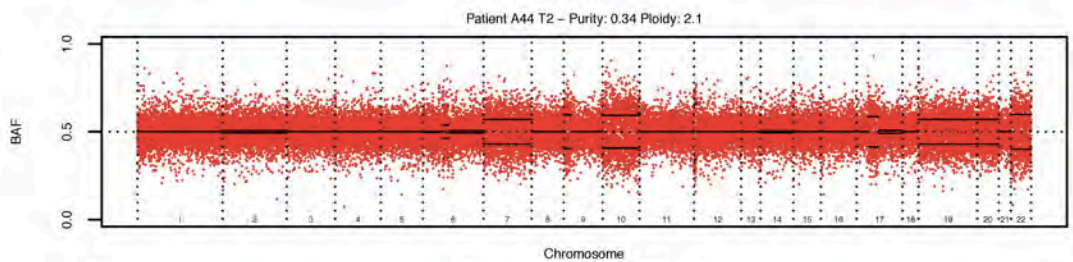

Patient A44 S – Purity: 1 Ploidy: 2.05
LRR
Chromosome

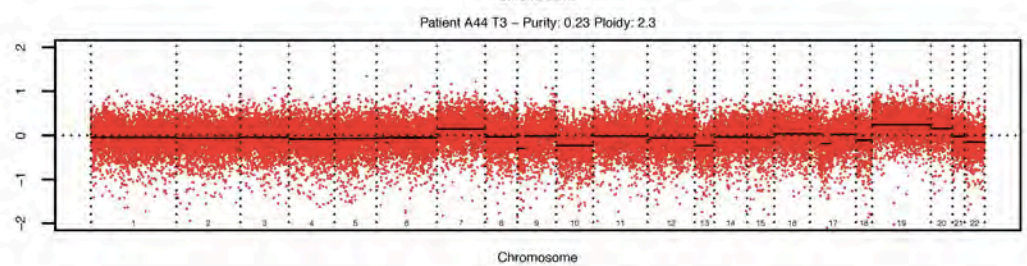

Patient A44 S – Purity: 1 Ploidy: 2.05
BAF
Chromosome

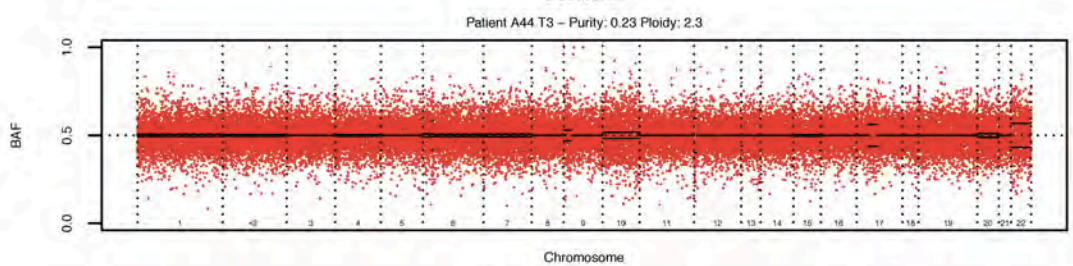

Patient A44 T1 – Purity: 0.6 Ploidy: 2.1
LRR
Chromosome

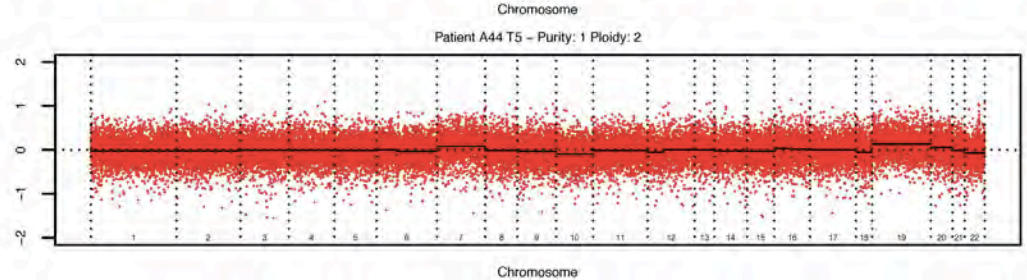

Patient A44 T1 – Purity: 0.6 Ploidy: 2.1
BAF
Chromosome

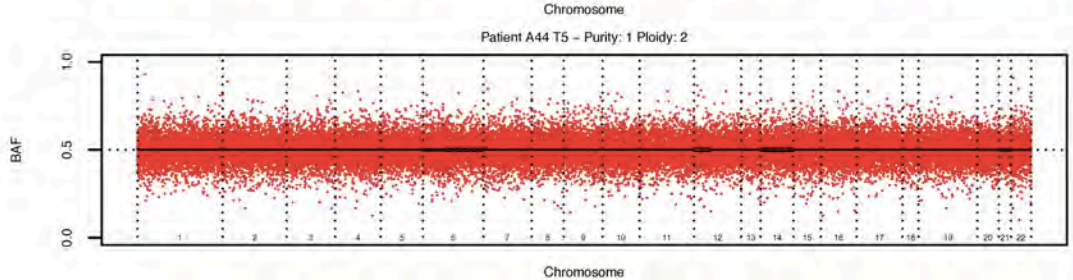

Patient A44 T2 – Purity: 0.34 Ploidy: 2.1
LRR
Chromosome

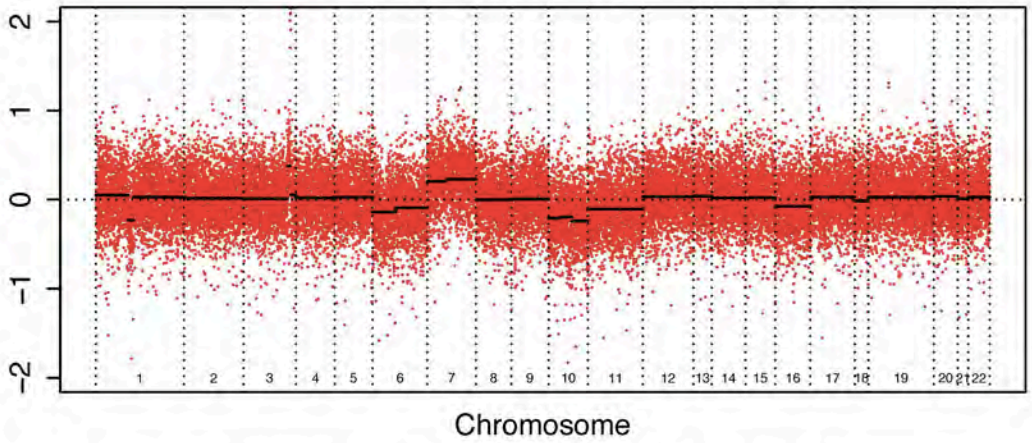

Patient A44 T2 – Purity: 0.34 Ploidy: 2.1
BAF
Chromosome

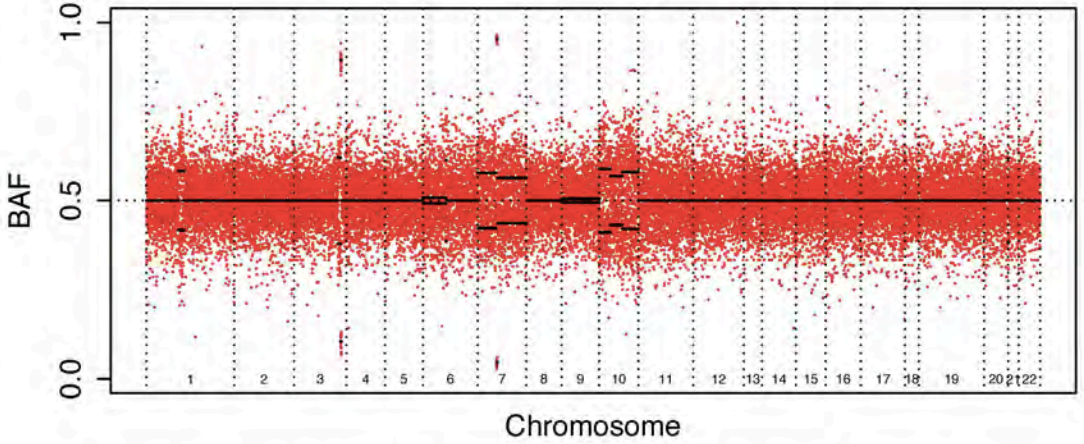

Patient A44 T3 – Purity: 0.23 Ploidy: 2.3
LRR
Chromosome

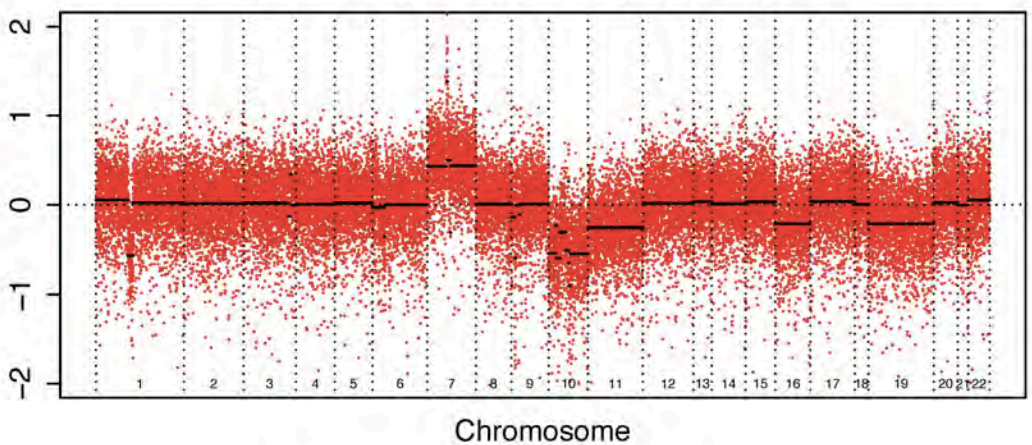

Patient A44 T3 – Purity: 0.23 Ploidy: 2.3
BAF
Chromosome

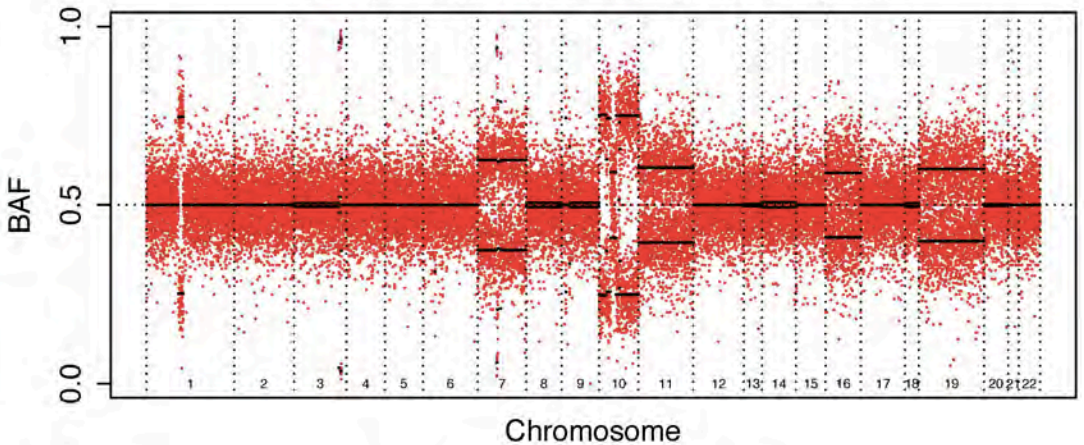

Patient A44 T5 – Purity: 1 Ploidy: 2
LRR
Chromosome

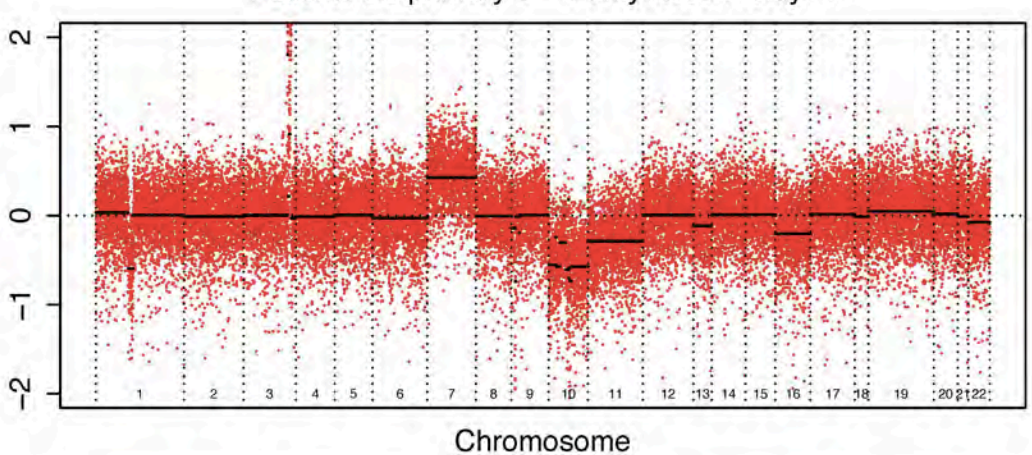

Patient A44 T5 – Purity: 1 Ploidy: 2
BAF
Chromosome

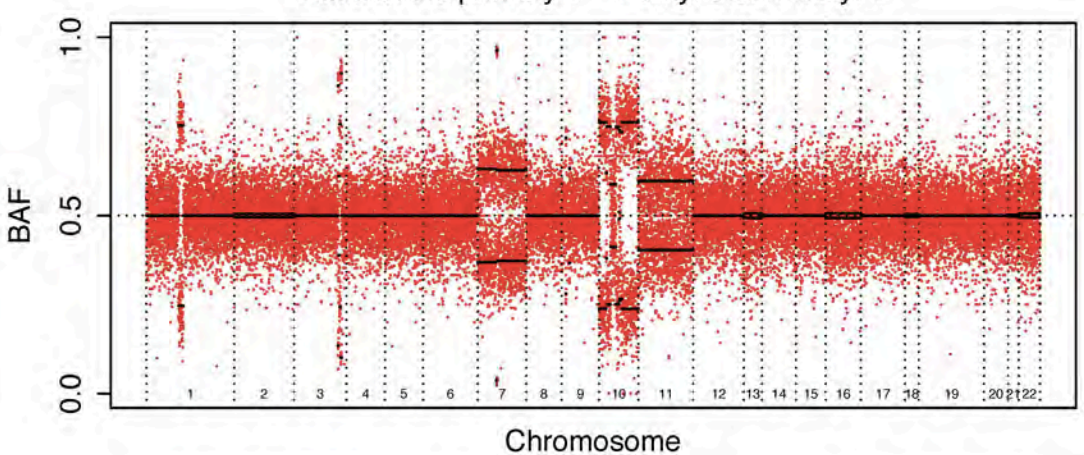

Patient A23 primary M – Purity: 0.18 Ploidy: 3.75
LRR
Chromosome

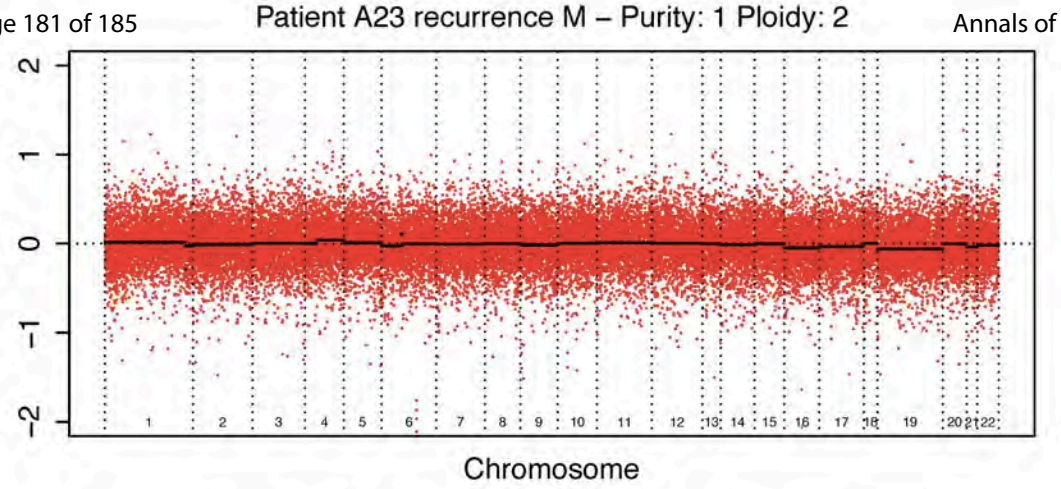

Patient A23 primary M – Purity: 0.18 Ploidy: 3.75
BAF
Chromosome

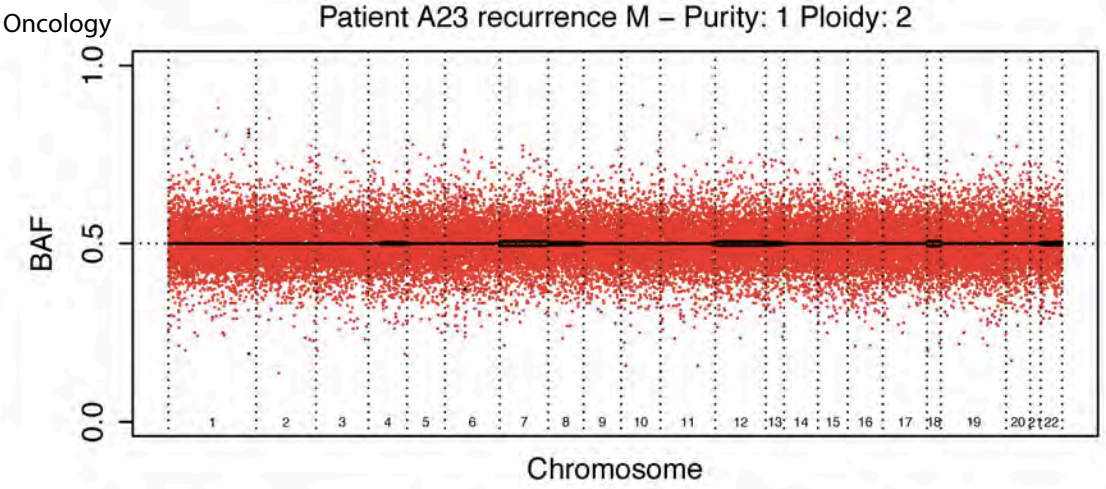

Patient A23 primary S – Purity: 0.5 Ploidy: 3.9
LRR
Chromosome

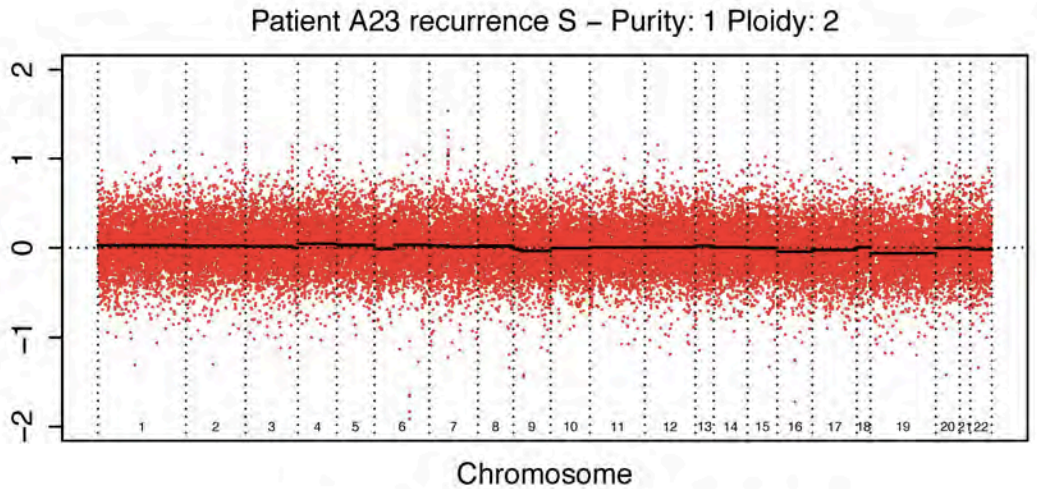

Patient A23 primary S – Purity: 0.5 Ploidy: 3.9
BAF
Chromosome

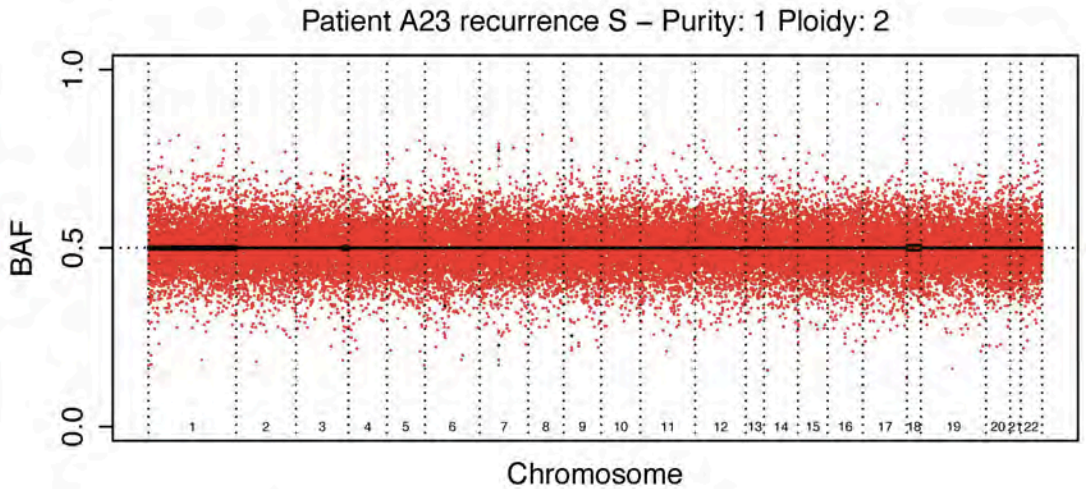

Patient A23 primary T – Purity: 0.52 Ploidy: 4
LRR
Chromosome

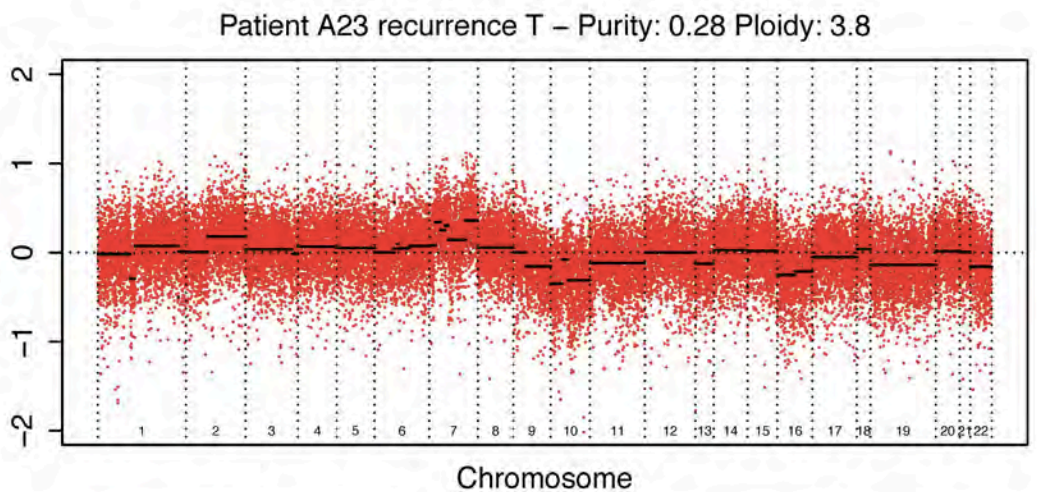

Patient A23 primary T – Purity: 0.52 Ploidy: 4
BAF
Chromosome

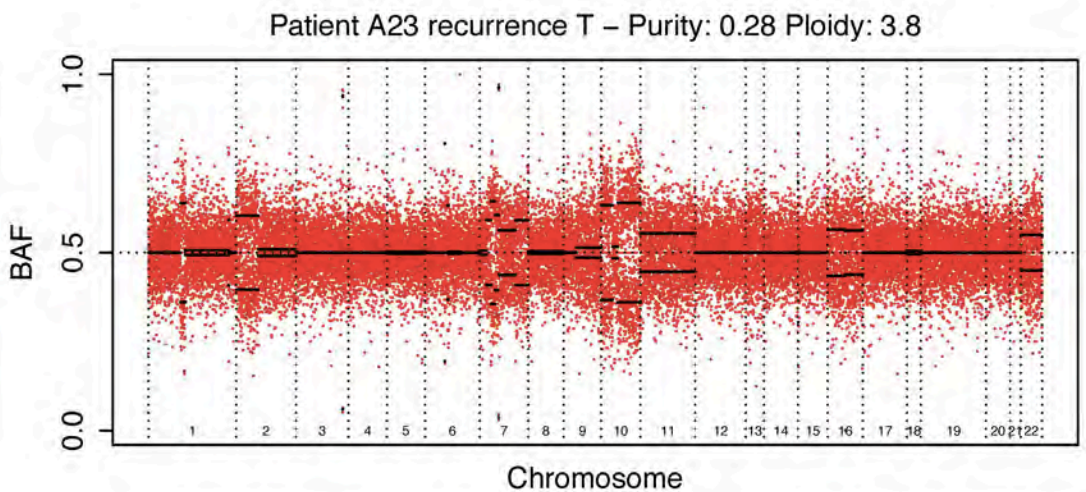

Patient A23 recurrence M – Purity: 1 Ploidy: 2
LRR
Chromosome

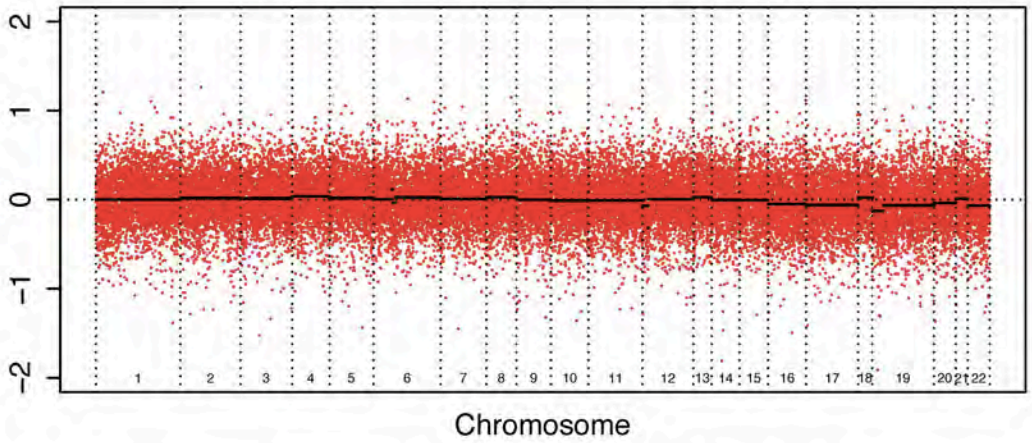

Patient A23 recurrence M – Purity: 1 Ploidy: 2
BAF
Chromosome

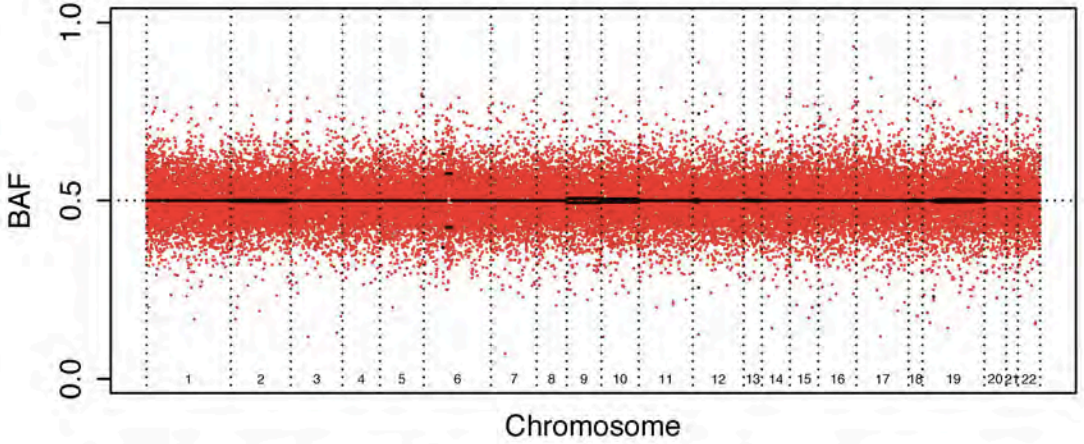

Patient A23 recurrence S – Purity: 1 Ploidy: 2
LRR
Chromosome

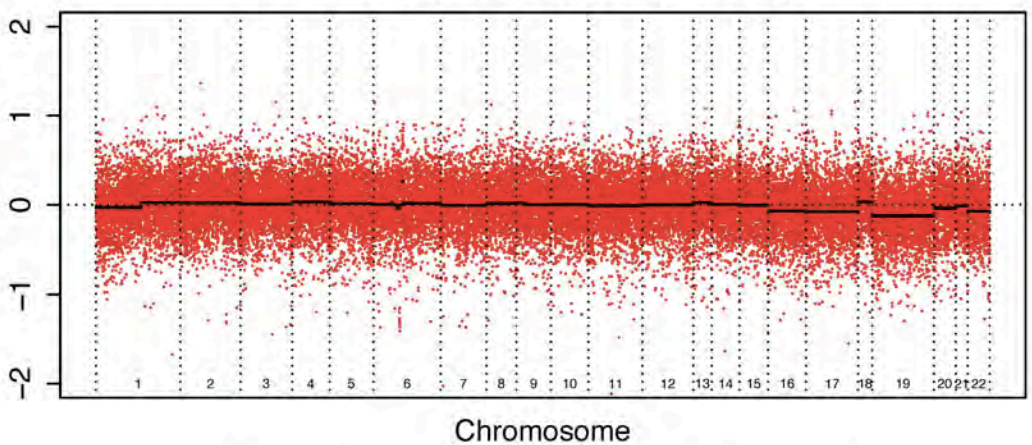

Patient A23 recurrence S – Purity: 1 Ploidy: 2
BAF
Chromosome

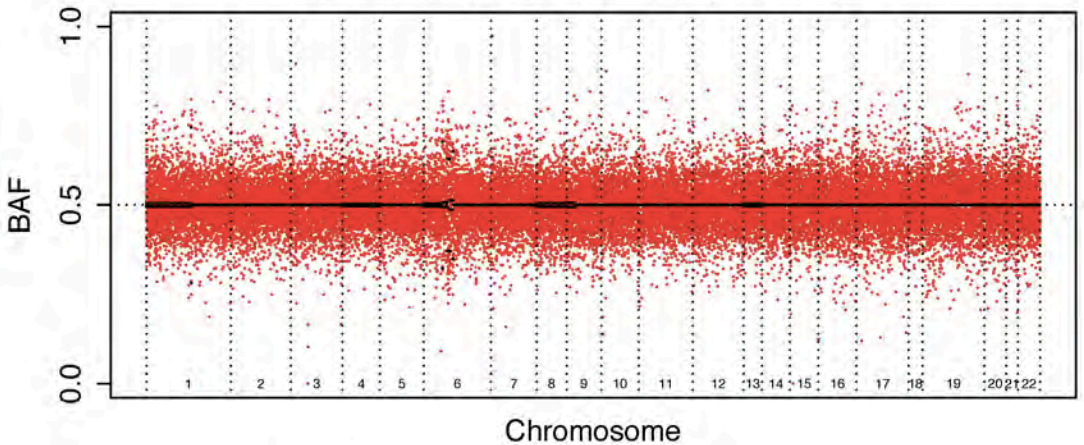

Patient A23 recurrence T – Purity: 0.28 Ploidy: 3.8
LRR
Chromosome

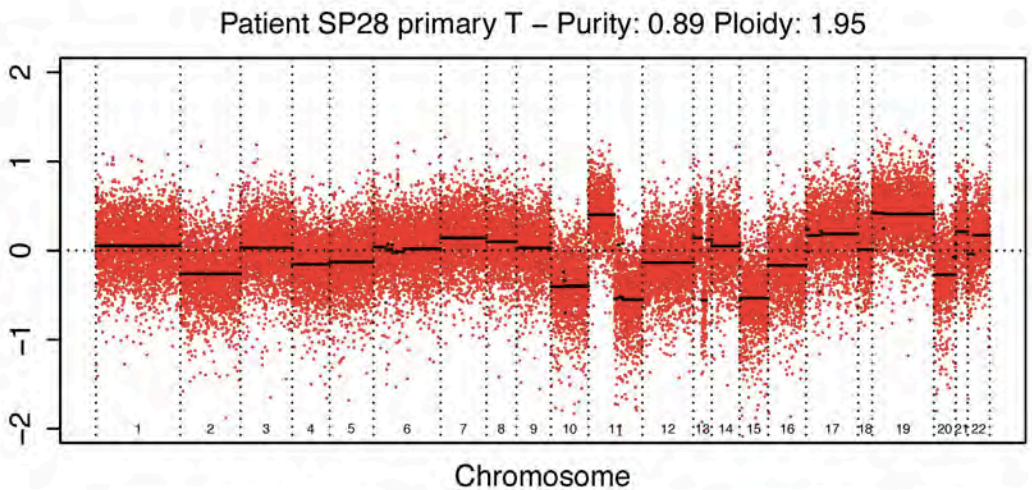

Patient A23 recurrence T – Purity: 0.28 Ploidy: 3.8
BAF
Chromosome

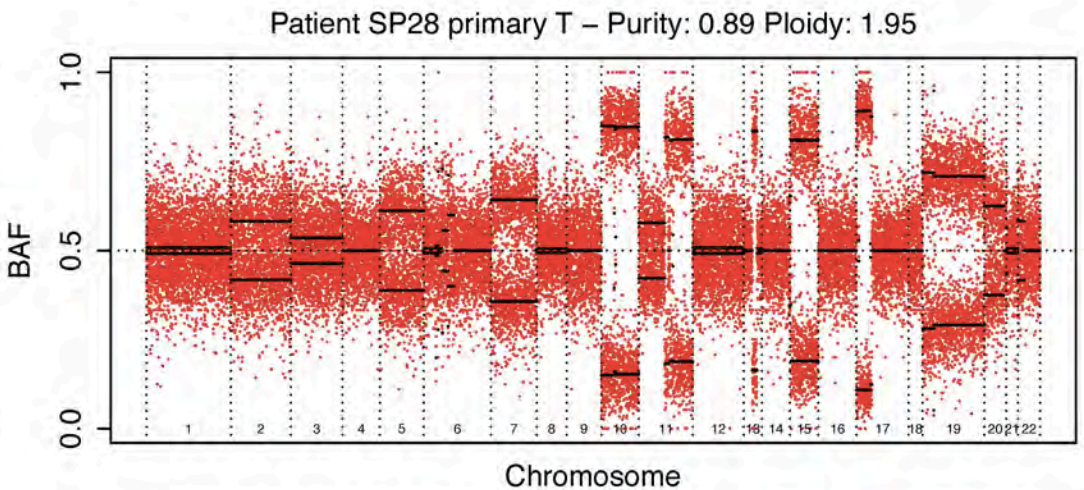

Patient SP28 primary M – Purity: 1 Ploidy: 2
LRR
Chromosome

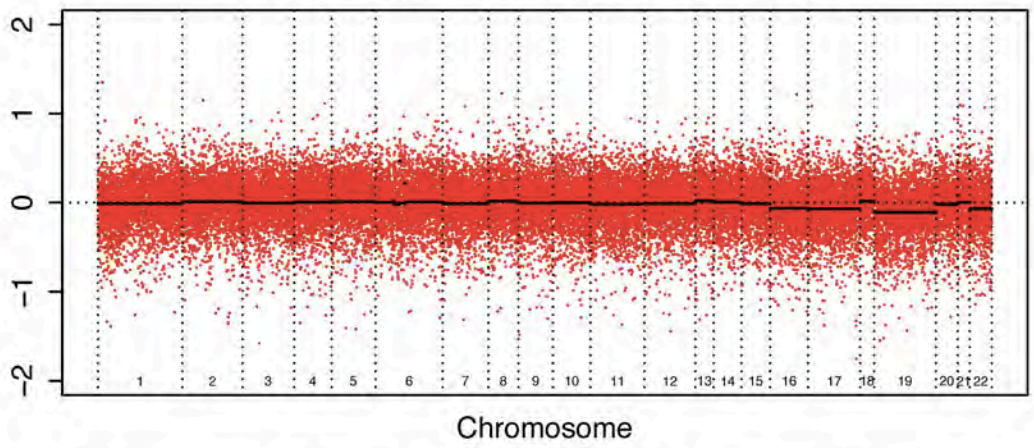

Patient SP28 primary M – Purity: 1 Ploidy: 2
BAF
Chromosome

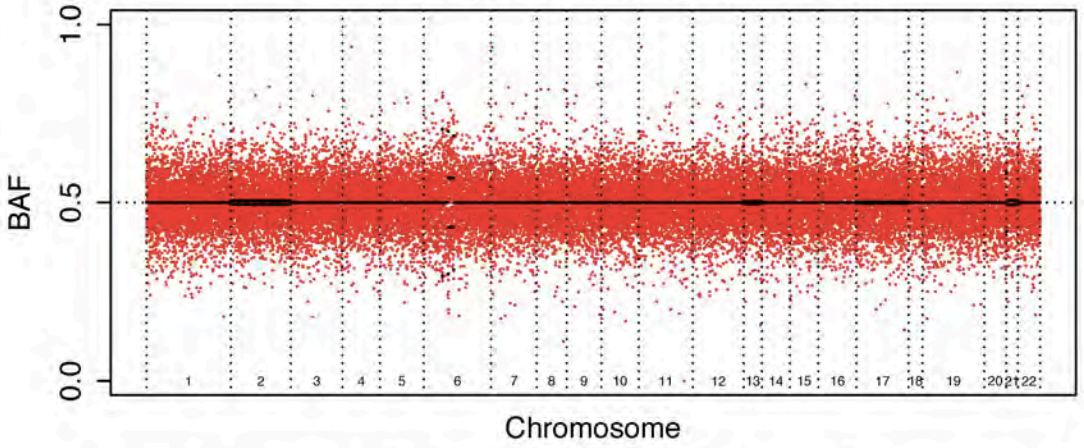

Patient SP28 primary S – Purity: 1 Ploidy: 2
LRR
Chromosome

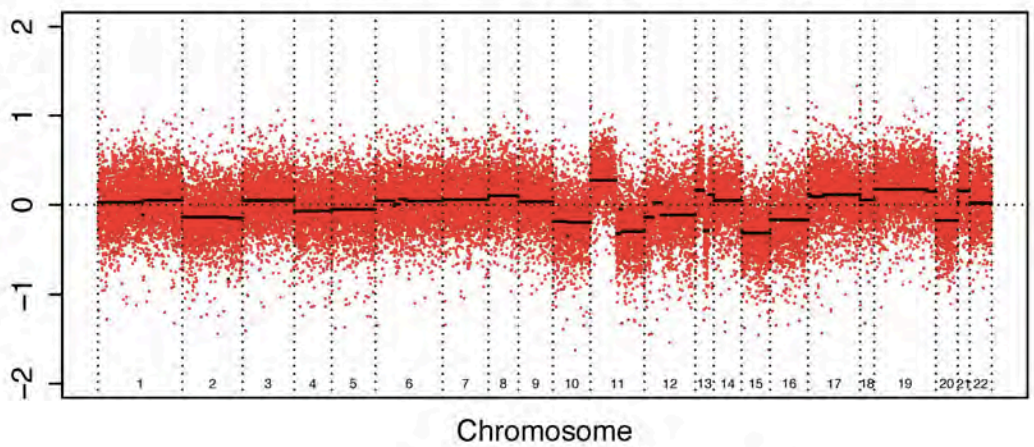

Patient SP28 primary S – Purity: 1 Ploidy: 2
BAF
Chromosome

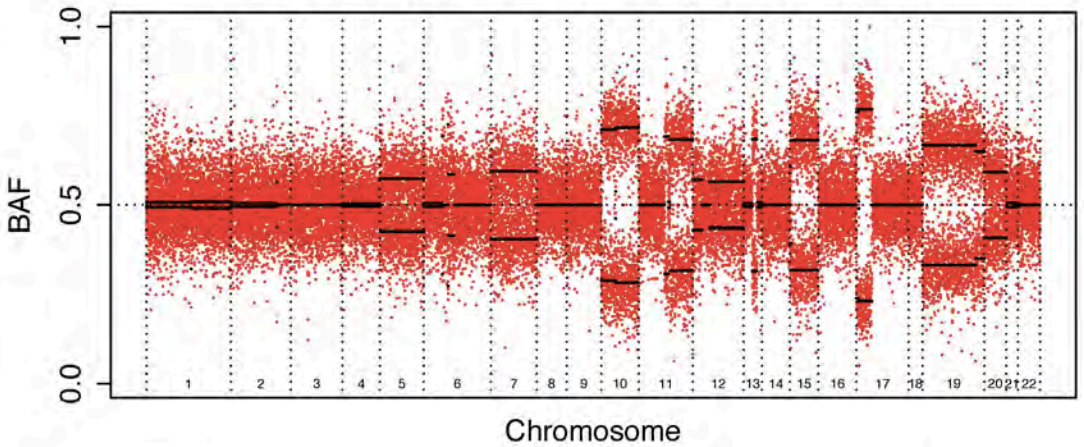

Patient SP28 primary T – Purity: 0.89 Ploidy: 1.95
LRR
Chromosome

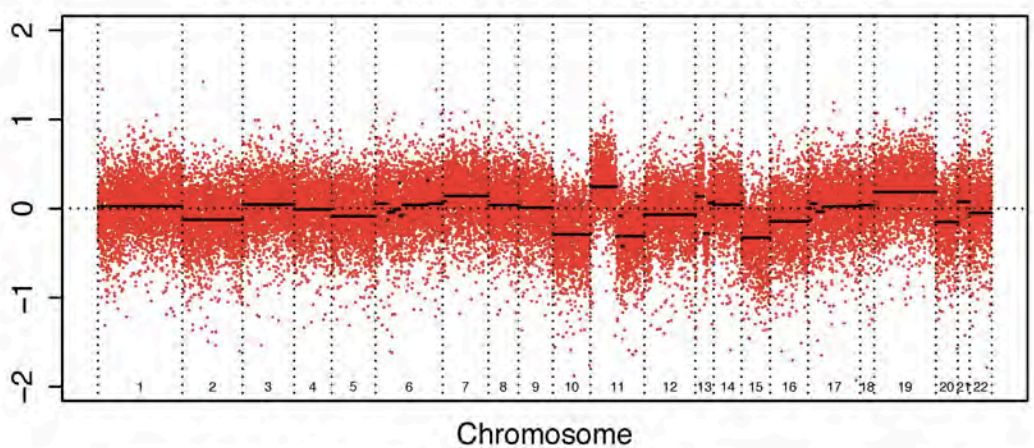

Patient SP28 primary T – Purity: 0.89 Ploidy: 1.95
BAF
Chromosome

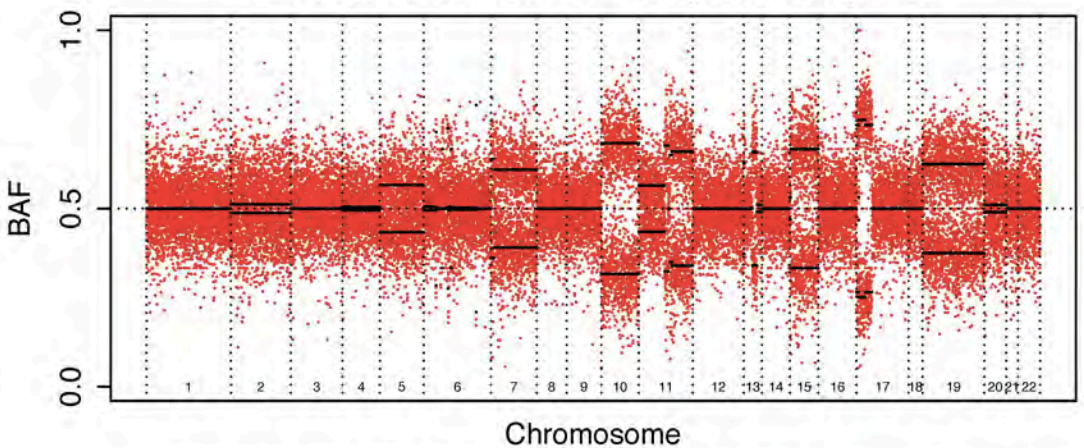

Patient SP28 recurrence M – Purity: 1 Ploidy: 2
LRR
Chromosome


Patient SP28 recurrence M – Purity: 1 Ploidy: 2
BAF
Chromosome

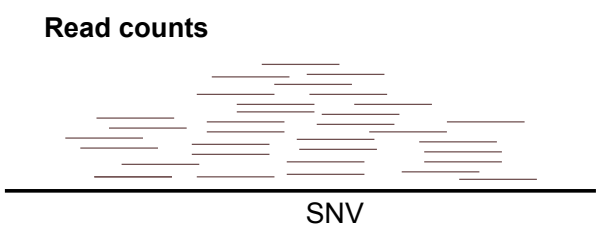

Patient SP28 recurrence S – Purity: 0.53 Ploidy: 1.85
LRR
Chromosome


Patient SP28 recurrence S – Purity: 0.53 Ploidy: 1.85
BAF
Chromosome


Patient SP28 recurrence T – Purity: 0.49 Ploidy: 1.95
LRR
Chromosome

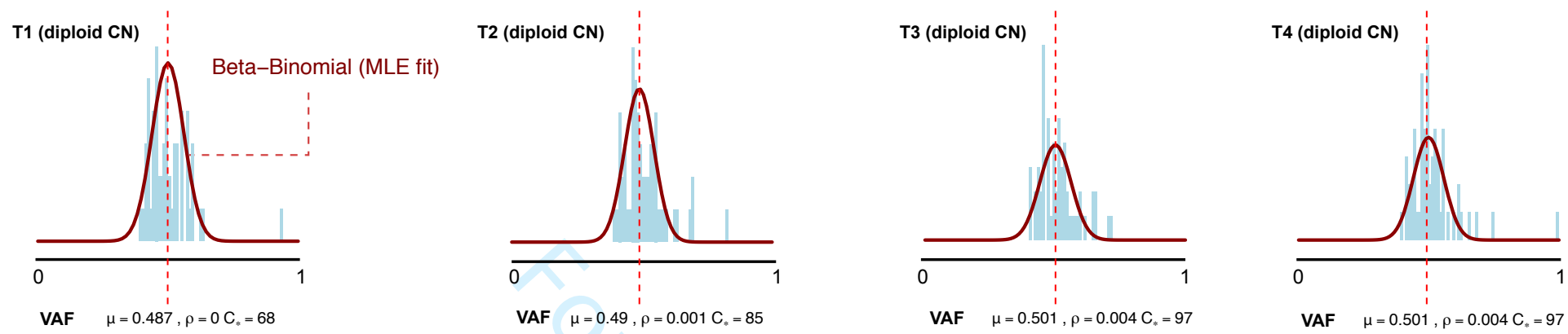

Patient SP28 recurrence T – Purity: 0.49 Ploidy: 1.95
BAF
Chromosome

A **PATIENT 52** — **Cancer Cell Fractions (CCF) from Whole Exome Sequencing of 4 primary tumour regions**



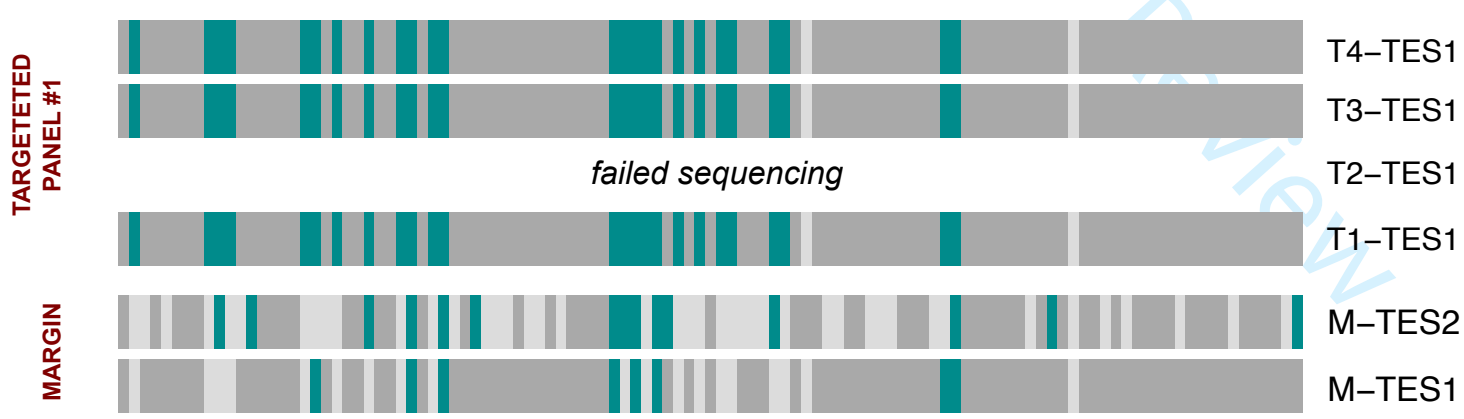
Clonal Mutations
- Exome regions
- SNVs (grouped by Copy Number status)
- CCF > 0.8 across **all** regions

B **Training model.** *Expected read counts harbouring a variant allele, for a clonal SNV (adjusted for Copy Number)*

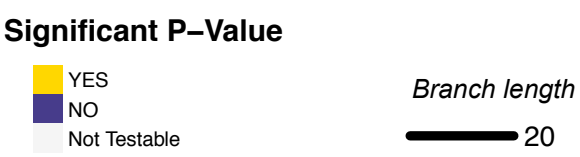


*Number of reads (NV)s with mutant alllele from a primary region with CN = **c**.*

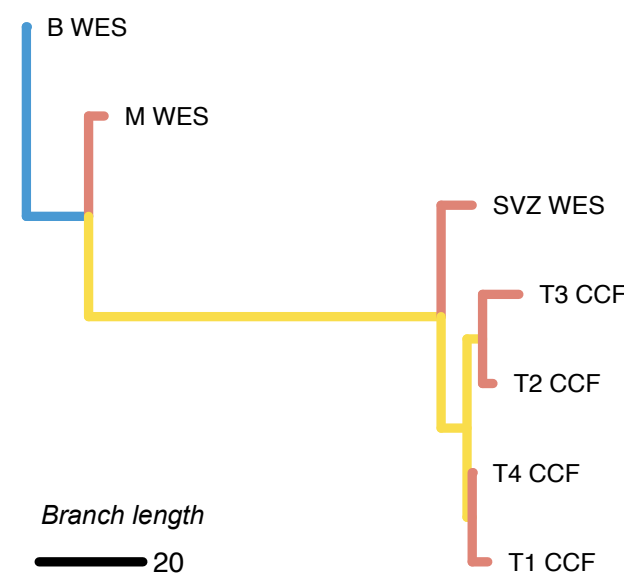
C **Test data.** *Deep Sequencing reveals clonal SNVs in the primary tumour that are missing in the margin samples.*



Testing for True Negatives with deep-sequenced SNVs with a low-purity tissue
- clonal SNVs with a suitable training set
- **worst-case purity** assumption of 1%



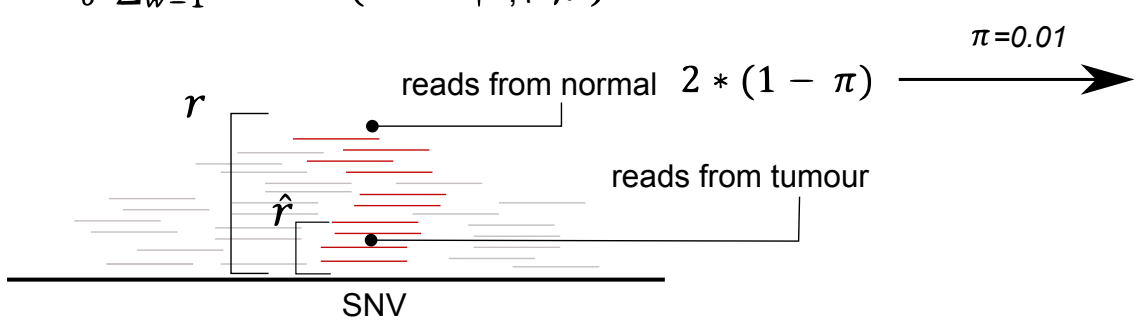
D **Phylogenetic analysis.** *The tree supports margin samples being ancestral to primary tumour regions.*



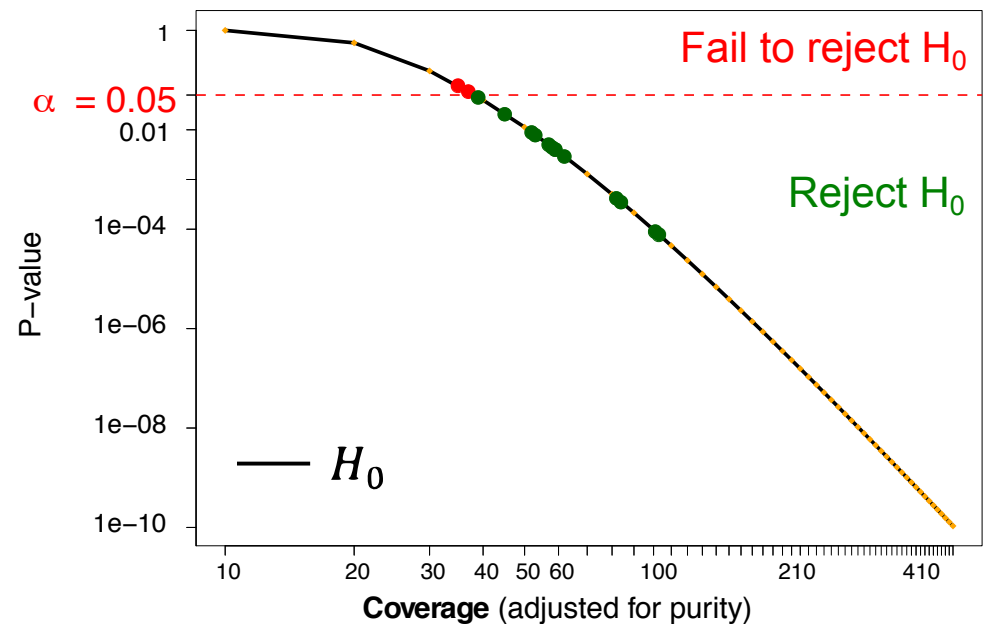
E **Deep-resolution clonal SNVs (~*3000x*)**

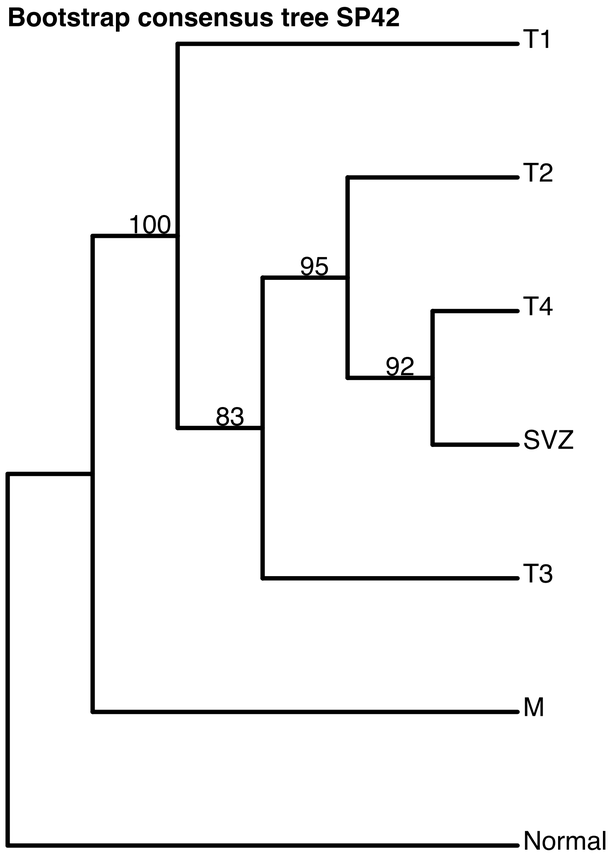
NV < k in M; tested with read coverage from tumour (NR).

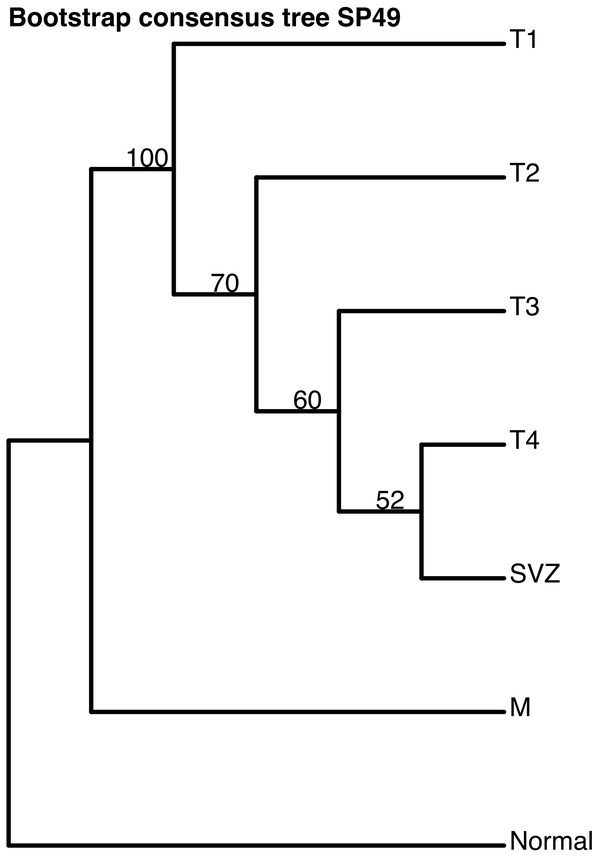
$$H_0: \sum_{w=1}^{k} \text{BetaBin}(v = w | \hat{r}; \mu, \rho).$$

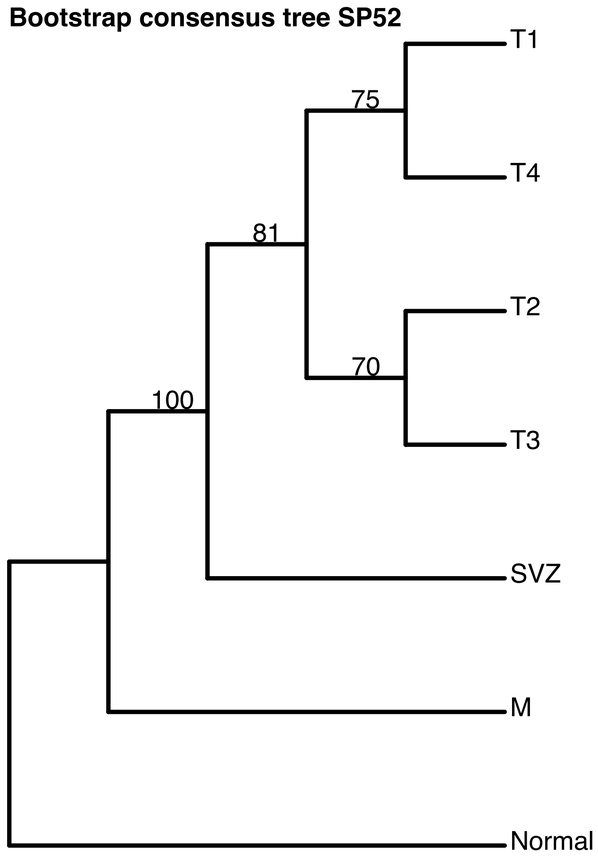


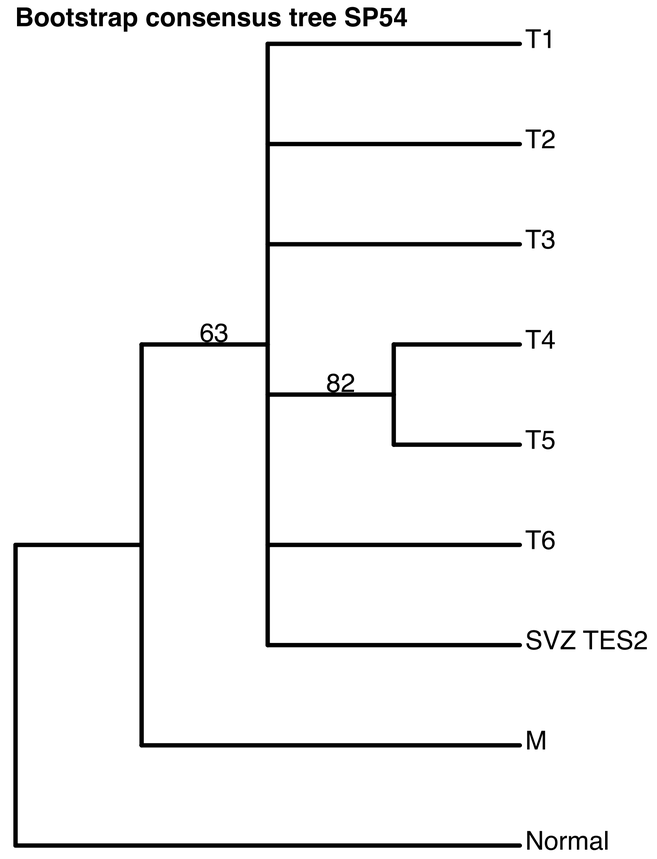
Test power for μ = 0.5 and ρ =5 x 10^{-2} *at significance level* α = 0.05

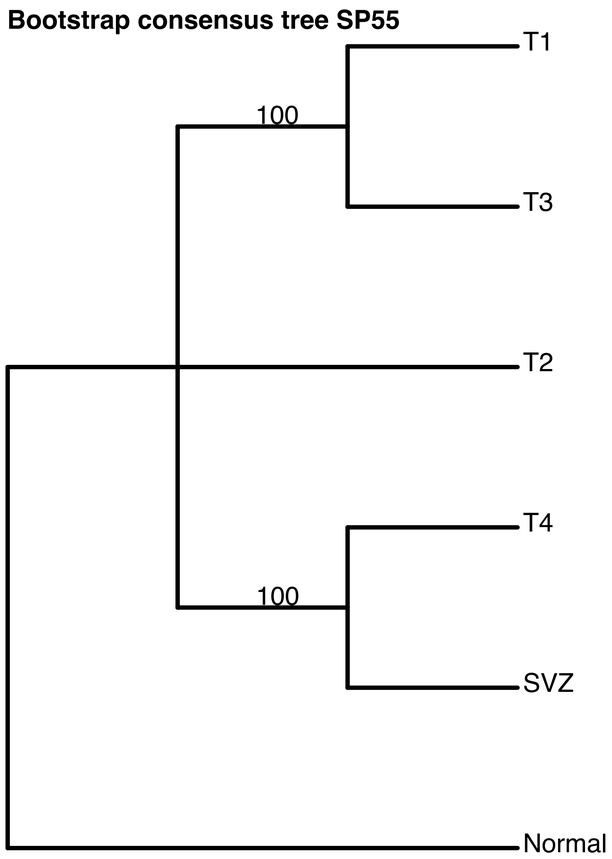


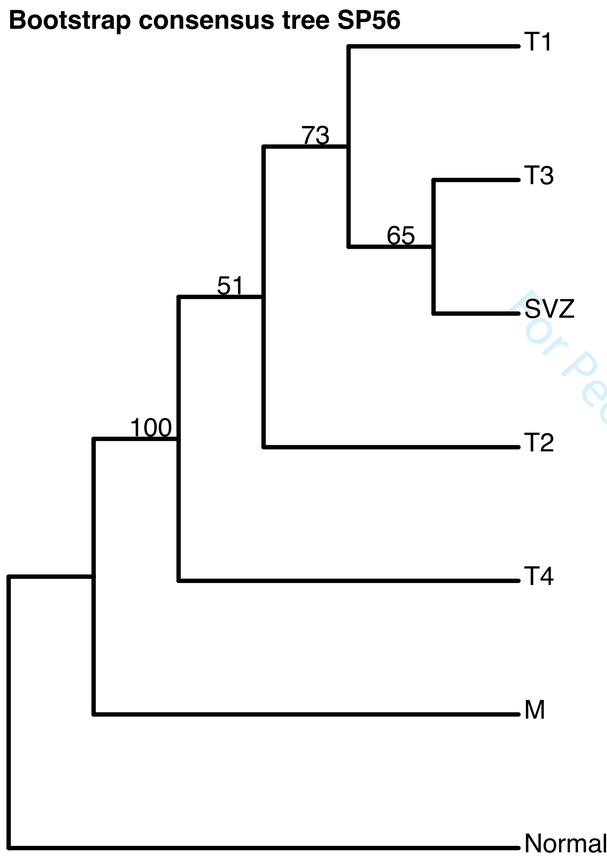


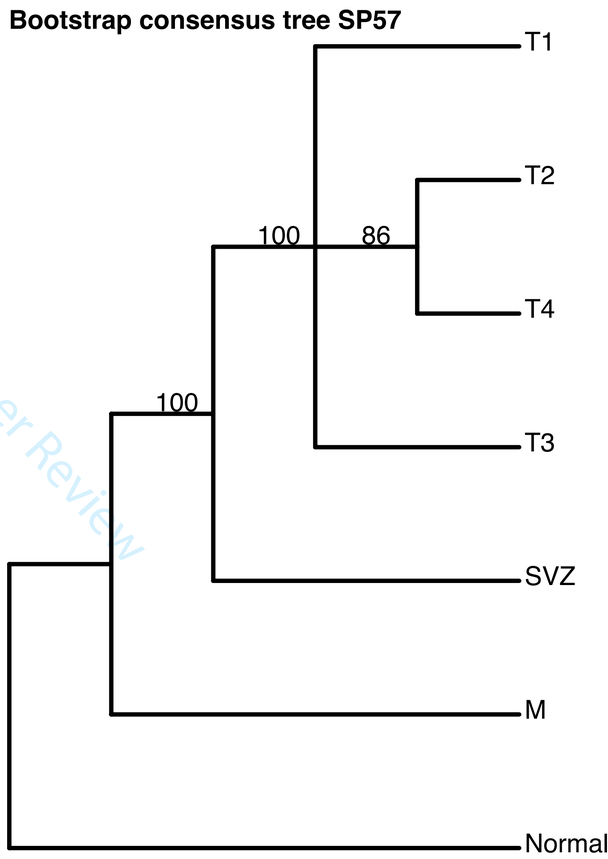


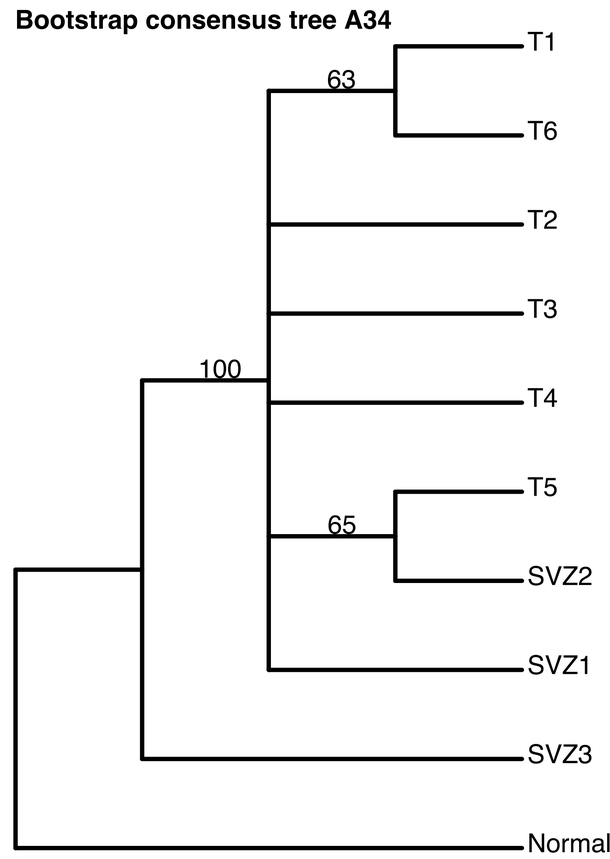


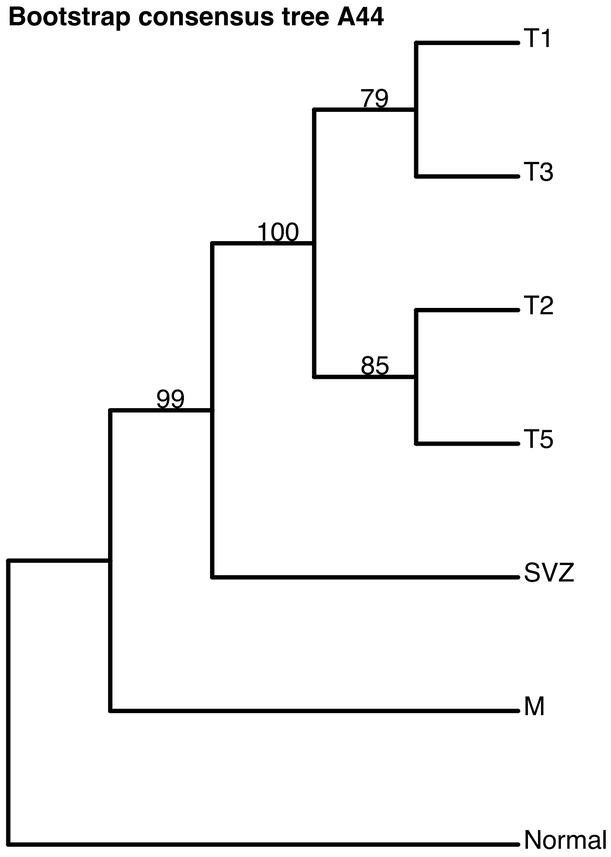


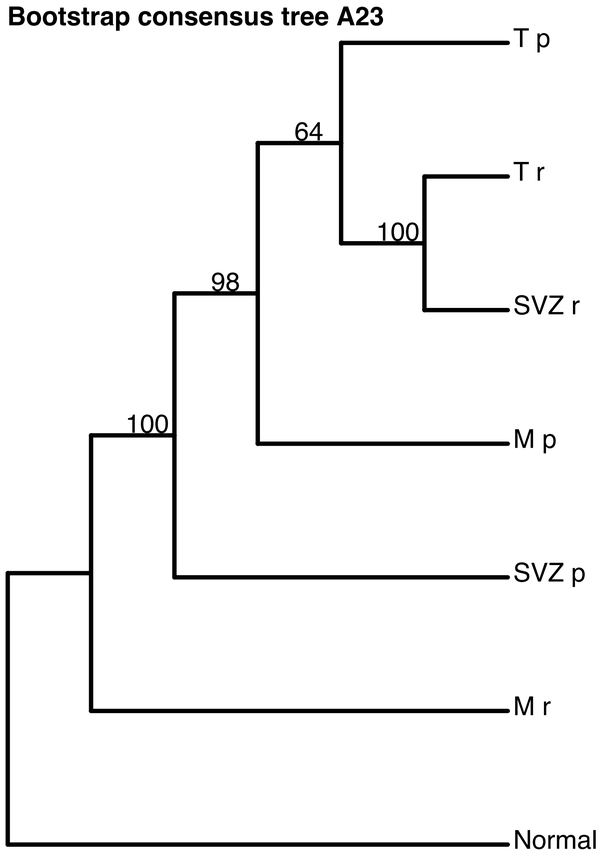


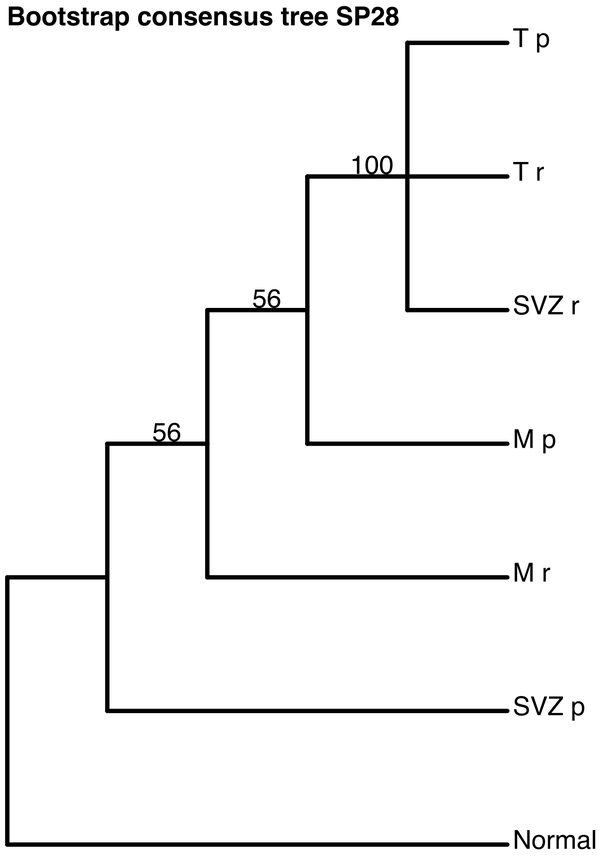








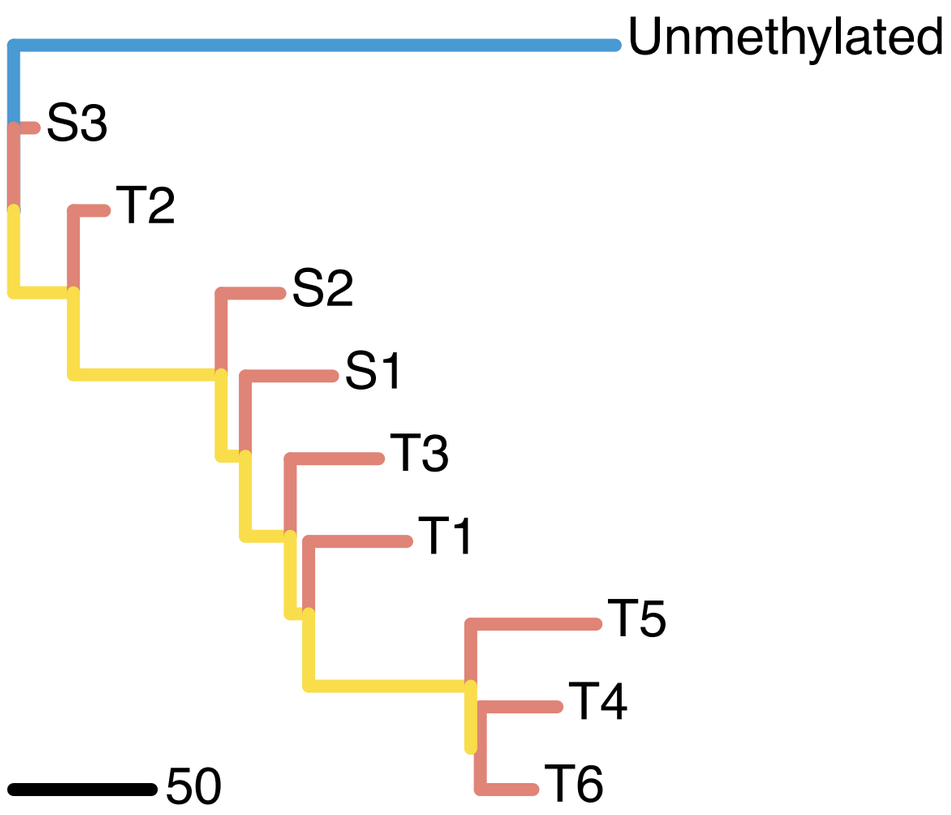


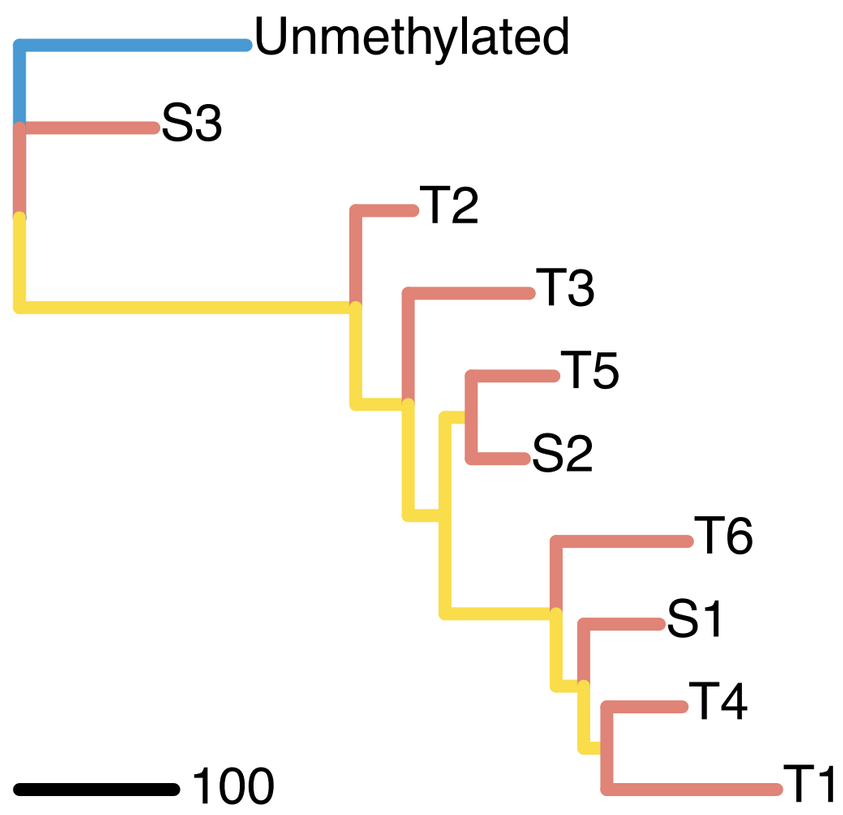


IRX2

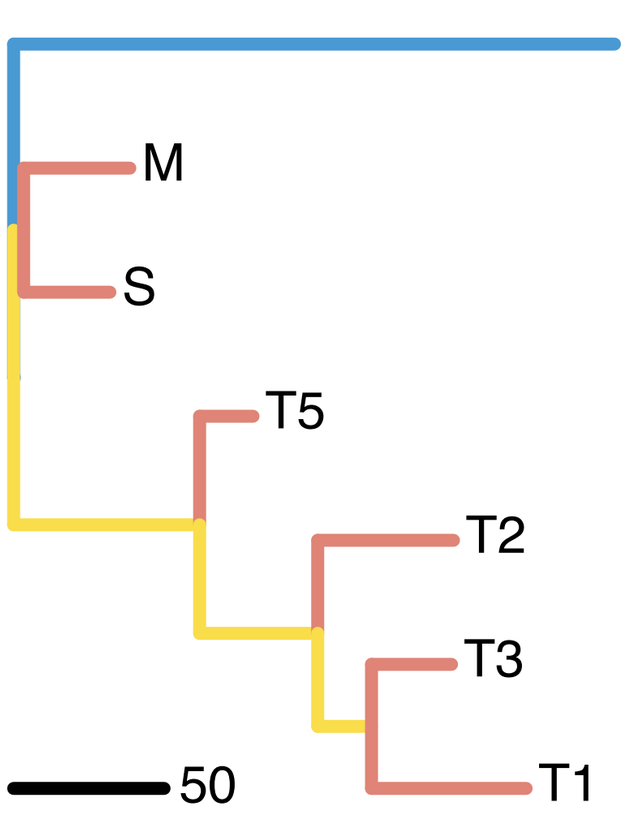
NETO1

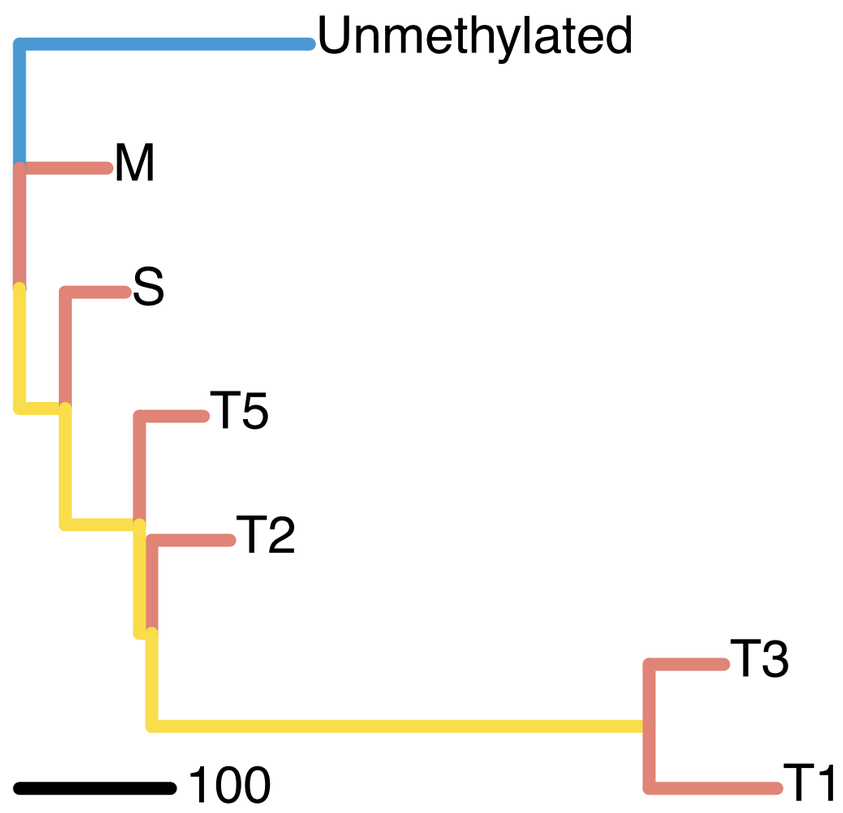
A34





A44





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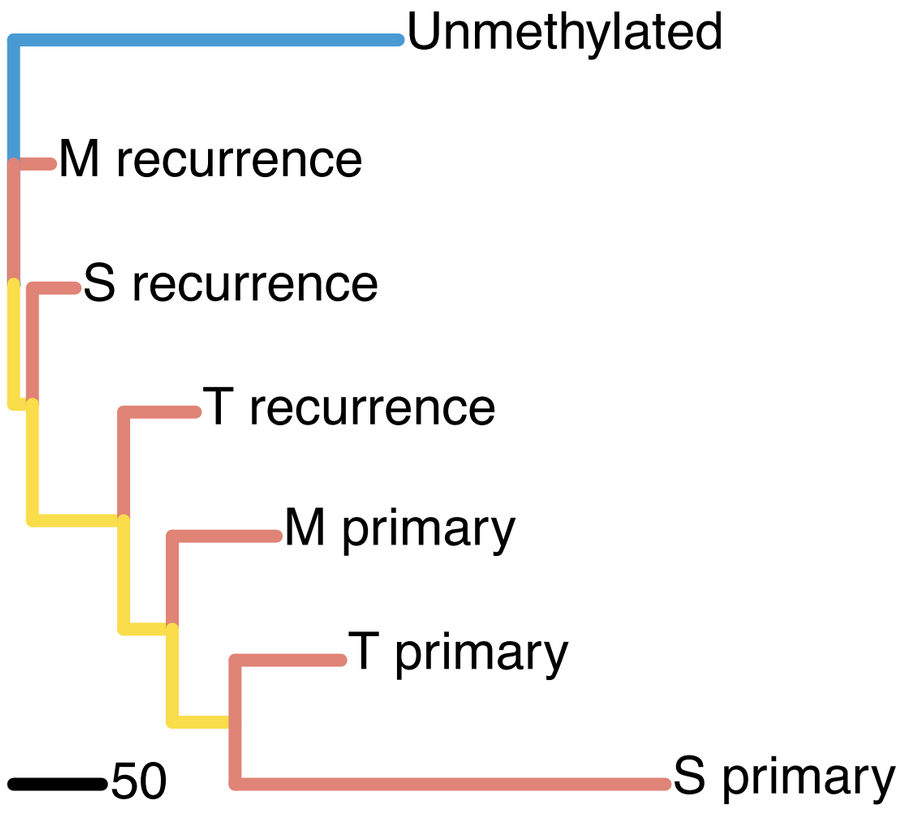

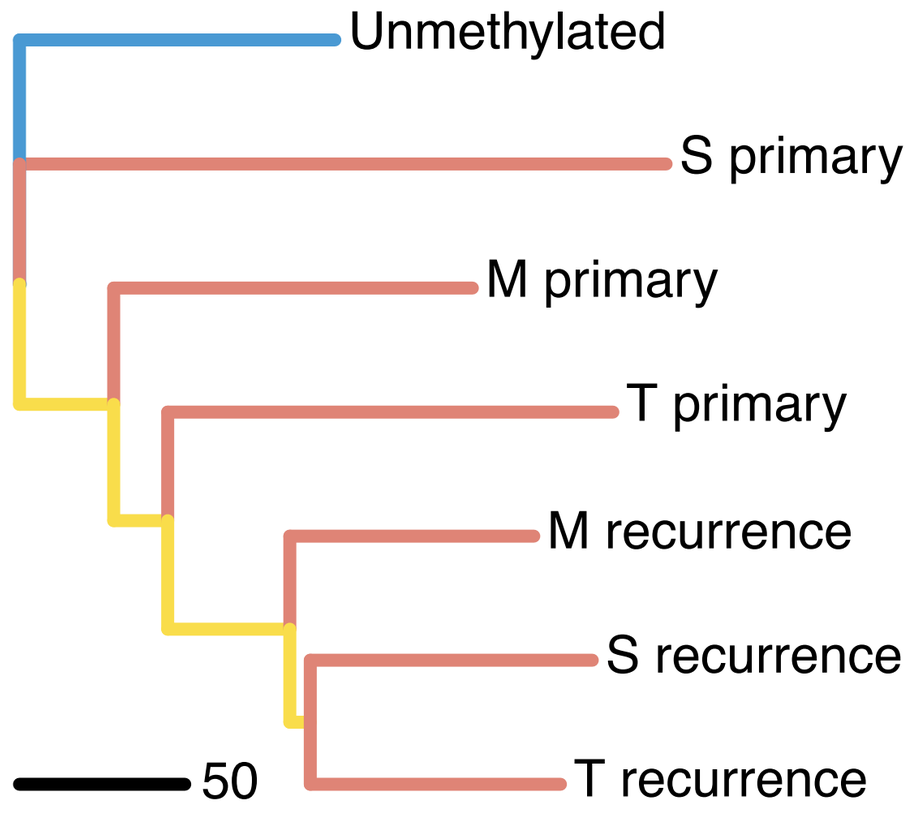

SP28